



SEQUENCE LISTING

<110> Anderson, David
Burgess, Catherine
Casman, Stacie
Colman, Steven
Edinger, Shlomit R.
Ellerman, Karen
Gerlach, Valerie
Gunther, Erik
Kekuda, Ramesh
MacDougall, John R.
Mehrabian, Fuad
Patturajan, Meera
Rothenberg, Mark
Shimkets, Richard
Smithson, Glennda
Spytek, Kimberly A.
Stone, David J.
Vernet, Corine A.M.
Zerhusen, Bryan D.

<120> PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS OF
USING THE SAME

<130> 21402-250 (CURA-550)

<140> 10/052,648
<141> 2002-01-18

<150> 60/262,454
<151> 2001-01-18

<150> 60/272,920
<151> 2001-03-02

<150> 60/284,549
<151> 2001-04-18

<150> 60/303,229
<151> 2001-07-05

<150> 60/262,892
<151> 2001-01-19

<150> 60/263,605
<151> 2001-01-23

<150> 60/269,098

<151> 2001-02-15

<150> 60/264,159

<151> 2001-01-25

<150> 60/265,517

<151> 2001-01-31

<150> 60/271,855

<151> 2001-02-27

<150> 60/267,057

<151> 2001-02-07

<150> 60/286,287

<151> 2001-04-25

<160> 97

<170> PatentIn Ver. 2.1

<210> 1

<211> 3063

<212> DNA

<213> Homo sapiens

<400> 1

atgtcaccgc ctctgtgtcc ctccttctc ctggctgtgg gcctgcggct ggctggaact 60
ctcaacccca gtgatcccaa tacctgcagc ttctggaaa gcttcactac caccaccaag 120
gagtcccaact cccgcccctt cagcctgctc ccctcagagc cctgcgagcg gccctggag 180
ggcccccata cttgccccca gcccacggtt gtataccgga ccgtgtaccg tcaggtggtg 240
aagacggacc accggccagcg cctgcagtgc tgccatggct tctatgagag cagggggttc 300
tgtgtcccgc tctgtgcccc ggagtgtgtc catggccgtt gtgtggcacc caatcagtgc 360
caatgtgtgc caggctggcg gggcgcacac tggccagtg agtgtcccc agaatgtgg 420
gggccacagt gtgacaagcc ctgcagctgc ggcacacaaca gctcgtgtga tcccaagagt 480
ggggtatgtt cttgccttc tggctctgcag ccccgaaact gccttcagcc ctgtacccct 540
ggctactatg gccctgcctg ccagttccgc tgccagtgcc atggggcacc ctgcgtatccc 600
cagactggag cttgttctg ccccgcaag agaactgggc ccagctgtga cgtgtcctgt 660
tcccaggcga cttctggctt cttctgcccc agcacccatt cttgccaaaa tggaggtgtc 720
ttccaaaccc cacagggtctc ctgcagctgc cccctggct ggatggatg gagggtgggg 780
cctgtggcga tgggtgtgg gtctggggag aattctgtgg gtgggtctaa gcagggtctc 840
aagggcacca tctgtccct gccctgcca gagggcttc acggacccaa ctgctccag 900
gaatgtcgct gccacaacgg cggccctgt gaccgattca ctggcagtg ccgctgcgt 960
ccgggttaca ctggggatcg gtgcggggag gagtgcccg tggccgctt tggcaggac 1020
tgtgtgaga cgtgcgactg cggccggac gcccgttgc tcccgccaa cgccgcgt 1080
ctgtgcgaac acggcttcac tggggaccgc tgacacggatc gcctctgccc cgacggcttc 1140
tacggtctca gctgccaggc cccctgcacc tgcgaccggg agcacagcct cagctgccac 1200

ccgatgaacg gggagtgctc ctgcctgccg ggctggcg ggctccactg caacgagagc 1260
 tccccgcagg acacgcattgg gcccagggtgc caggagact gtctctgcct gcacgggtgc 1320
 gtctgcagg ctaccagcgg cctctgtcag tgcgcggg gttacacggg ccctcactgt 1380
 gctagtcttt gtcctcctga cacctacggt gtcaactgtt ctgcacgctg ctcatgtgaa 1440
 aatgccatcg cctgctcacc catcgacggc gagtgctgc gcaaggaagg ttggcagcgt 1500
 ggttaactgtctggtccctg cccacccggaa acctggggct tcagttgcaaa tgccagctgc 1560
 cagtgtgccc atgaggcagt ctgcagcccc caaactggag cctgtacctg caccctggg 1620
 tggcatgggg cccactgcca gctgcccgtt ccgaaggggc agtttgagaa agtttgcc 1680
 agtcgctgtg actgtgacca ctctgatggc tggaccctg ttcatggacg ctgtcagtgc 1740
 caggctggct ggatgggtgc ccgctgcccc ctgctgcctgc ctgaggcctt atggggagtc 1800
 aactgttagca acacctgcac ctgcaagaat gggggcacct gtctccctga gaatggcaac 1860
 tgcgtgtgtg caccggatt ccggggcccc tcctgccaga gatcctgtca gcctggccgc 1920
 tatggcaaac gctgtgtgcc ctgcaagtgc gctaaccact cttctgcca cccctcgaac 1980
 gggacactgt actgcctggc tggctggaca ggccccgact gctcccagcg ctgccccttg 2040
 gggacatttg gtgctaactg ctcccagcca tgccagtggt gtcctggaga aaagtggcac 2100
 ccagagactg gggcctgtgt atgtcccca gggcacagtg gtgcacccctg caggattgga 2160
 atccaggagc ccttactgt gatgccgacc actccagtag cgtataactc gtcgggtgca 2220
 gtgattggca ttgcagtgt ggggtccctt gtgttagccc tggtaggcact gttcattggc 2280
 tatcggcaact ggcaaaaagg caaggagcac caccacctgg ctgtggctta cagcagcggg 2340
 cgcctggacg gctccgagta tgcataccca gatgtccctc ccagctacag tcactactac 2400
 tccaacccca gctaccacac cctgtcgca gatgtccctc ccctaaacaag 2460
 gttccaggcc cgctcttgc cagcctgca gatgtccctc ccctaaacaag 2460
 catgataacc acaccaccct gcctgctgac tggaaagcacc gccgggagcc ccctccaggg 2580
 cctctggaca gggggagcag ccgcctgac cgaagctaca gctataacta cagcaatggc 2640
 ccaggcccat tctacaataa agggctcatc tctgaagagg agctcggggc cagtgtggct 2700
 tccctgagca gtgagaaccc atatgccacc atccgggacc tgcccagctt gccagggggc 2760
 ccccgggaga gcagctacat ggagatgaaa ggcctccct caggatctcc ccccaggcag 2820
 cctcctcaat tctggacag ccagaggcgg cggcaacccc agccacagag agacagtggc 2880
 acctacgagc agccagcccc cctgatccat gaccgagact ctgtgggctc ccagccccc 2940
 ctgcctccgg gcctacccccc cggccactat gactcacca agaacagcca catccctgga 3000
 cattatgact tgcctccagt acggcatccc ccatcacctc cacttcgacg ccaggaccgt 3060
 tga 3063

<210> 2
 <211> 1020
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Ser Pro Pro Leu Cys Pro Leu Leu Leu Leu Ala Val Gly Leu Arg
 1 5 10 15

Leu Ala Gly Thr Leu Asn Pro Ser Asp Pro Asn Thr Cys Ser Phe Trp
 20 25 30

Glu Ser Phe Thr Thr Thr Lys Glu Ser His Ser Arg Pro Phe Ser
 35 40 45

Leu Leu Pro Ser Glu Pro Cys Glu Arg Pro Trp Glu Gly Pro His Thr
50 55 60

Cys Pro Gln Pro Thr Val Val Tyr Arg Thr Val Tyr Arg Gln Val Val
65 70 75 80

Lys Thr Asp His Arg Gln Arg Leu Gln Cys Cys His Gly Phe Tyr Glu
85 90 95

Ser Arg Gly Phe Cys Val Pro Leu Cys Ala Gln Glu Cys Val His Gly
100 105 110

Arg Cys Val Ala Pro Asn Gln Cys Gln Cys Val Pro Gly Trp Arg Gly
115 120 125

Asp Asp Cys Ser Ser Glu Cys Ala Pro Gly Met Trp Gly Pro Gln Cys
130 135 140

Asp Lys Pro Cys Ser Cys Gly Asn Asn Ser Ser Cys Asp Pro Lys Ser
145 150 155 160

Gly Val Cys Ser Cys Pro Ser Gly Leu Gln Pro Pro Asn Cys Leu Gln
165 170 175

Pro Cys Thr Pro Gly Tyr Tyr Gly Pro Ala Cys Gln Phe Arg Cys Gln
180 185 190

Cys His Gly Ala Pro Cys Asp Pro Gln Thr Gly Ala Cys Phe Cys Pro
195 200 205

Ala Glu Arg Thr Gly Pro Ser Cys Asp Val Ser Cys Ser Gln Gly Thr
210 215 220

Ser Gly Phe Phe Cys Pro Ser Thr His Ser Cys Gln Asn Gly Gly Val
225 230 235 240

Phe Gln Thr Pro Gln Gly Ser Cys Ser Cys Pro Pro Gly Trp Met Val
245 250 255

Trp Arg Val Gly Pro Val Gly Met Gly Cys Gly Ser Gly Glu Asn Ser
260 265 270

Val Gly Gly Ala Lys Gln Gly Ser Lys Gly Thr Ile Cys Ser Leu Pro
275 280 285

Cys Pro Glu Gly Phe His Gly Pro Asn Cys Ser Gln Glu Cys Arg Cys
290 295 300

His Asn Gly Gly Leu Cys Asp Arg Phe Thr Gly Gln Cys Arg Cys Ala
305 310 315 320

Pro Gly Tyr Thr Gly Asp Arg Cys Arg Glu Glu Cys Pro Val Gly Arg
325 330 335

Phe Gly Gln Asp Cys Ala Glu Thr Cys Asp Cys Ala Pro Asp Ala Arg
340 345 350

Cys Phe Pro Ala Asn Gly Ala Cys Leu Cys Glu His Gly Phe Thr Gly
355 360 365

Asp Arg Cys Thr Asp Arg Leu Cys Pro Asp Gly Phe Tyr Gly Leu Ser
370 375 380

Cys Gln Ala Pro Cys Thr Cys Asp Arg Glu His Ser Leu Ser Cys His
385 390 395 400

Pro Met Asn Gly Glu Cys Ser Cys Leu Pro Gly Trp Ala Gly Leu His
405 410 415

Cys Asn Glu Ser Cys Pro Gln Asp Thr His Gly Pro Gly Cys Gln Glu
420 425 430

His Cys Leu Cys Leu His Gly Val Cys Gln Ala Thr Ser Gly Leu
435 440 445

Cys Gln Cys Ala Pro Gly Tyr Thr Gly Pro His Cys Ala Ser Leu Cys
450 455 460

Pro Pro Asp Thr Tyr Gly Val Asn Cys Ser Ala Arg Cys Ser Cys Glu
465 470 475 480

Asn Ala Ile Ala Cys Ser Pro Ile Asp Gly Glu Cys Val Cys Lys Glu
485 490 495

Gly Trp Gln Arg Gly Asn Cys Ser Val Pro Cys Pro Pro Gly Thr Trp
500 505 510

Gly Phe Ser Cys Asn Ala Ser Cys Gln Cys Ala His Glu Ala Val Cys
515 520 525

Ser Pro Gln Thr Gly Ala Cys Thr Cys Thr Pro Gly Trp His Gly Ala
530 535 540

His Cys Gln Leu Pro Cys Pro Lys Gly Gln Phe Gly Glu Gly Cys Ala
545 550 555 560

Ser Arg Cys Asp Cys Asp His Ser Asp Gly Cys Asp Pro Val His Gly
565 570 575

Arg Cys Gln Cys Gln Ala Gly Trp Met Gly Ala Arg Cys His Leu Ser
580 585 590

Cys Pro Glu Gly Leu Trp Gly Val Asn Cys Ser Asn Thr Cys Thr Cys
595 600 605

Lys Asn Gly Gly Thr Cys Leu Pro Glu Asn Gly Asn Cys Val Cys Ala
610 615 620

Pro Gly Phe Arg Gly Pro Ser Cys Gln Arg Ser Cys Gln Pro Gly Arg
625 630 635 640

Tyr Gly Lys Arg Cys Val Pro Cys Lys Cys Ala Asn His Ser Phe Cys
645 650 655

His Pro Ser Asn Gly Thr Cys Tyr Cys Leu Ala Gly Trp Thr Gly Pro
660 665 670

Asp Cys Ser Gln Arg Cys Pro Leu Gly Thr Phe Gly Ala Asn Cys Ser
675 680 685

Gln Pro Cys Gln Cys Gly Pro Gly Glu Lys Cys His Pro Glu Thr Gly
690 695 700

Ala Cys Val Cys Pro Pro Gly His Ser Gly Ala Pro Cys Arg Ile Gly
705 710 715 720

Ile Gln Glu Pro Phe Thr Val Met Pro Thr Thr Pro Val Ala Tyr Asn
725 730 735

Ser Leu Gly Ala Val Ile Gly Ile Ala Val Leu Gly Ser Leu Val Val
740 745 750

Ala Leu Val Ala Leu Phe Ile Gly Tyr Arg His Trp Gln Lys Gly Lys
755 760 765

Glu His His His Leu Ala Val Ala Tyr Ser Ser Gly Arg Leu Asp Gly
770 775 780

Ser Glu Tyr Val Met Pro Asp Val Pro Pro Ser Tyr Ser His Tyr Tyr
785 790 795 800

Ser Asn Pro Ser Tyr His Thr Leu Ser Gln Cys Ser Pro Asn Pro Pro
805 810 815

Pro Pro Asn Lys Val Pro Gly Pro Leu Phe Ala Ser Leu Gln Lys Pro
 820 825 830

 Glu Arg Pro Gly Gly Ala Gln Gly His Asp Asn His Thr Thr Leu Pro
 835 840 845

 Ala Asp Trp Lys His Arg Arg Glu Pro Pro Pro Gly Pro Leu Asp Arg
 850 855 860

 Gly Ser Ser Arg Leu Asp Arg Ser Tyr Ser Tyr Ser Tyr Ser Asn Gly
 865 870 875 880

 Pro Gly Pro Phe Tyr Asn Lys Gly Leu Ile Ser Glu Glu Glu Leu Gly
 885 890 895

 Ala Ser Val Ala Ser Leu Ser Ser Glu Asn Pro Tyr Ala Thr Ile Arg
 900 905 910

 Asp Leu Pro Ser Leu Pro Gly Gly Pro Arg Glu Ser Ser Tyr Met Glu
 915 920 925

 Met Lys Gly Pro Pro Ser Gly Ser Pro Pro Arg Gln Pro Pro Gln Phe
 930 935 940

 Trp Asp Ser Gln Arg Arg Arg Gln Pro Gln Pro Gln Arg Asp Ser Gly
 945 950 955 960

 Thr Tyr Glu Gln Pro Ser Pro Leu Ile His Asp Arg Asp Ser Val Gly
 965 970 975

 Ser Gln Pro Pro Leu Pro Pro Gly Leu Pro Pro Gly His Tyr Asp Ser
 980 985 990

 Pro Lys Asn Ser His Ile Pro Gly His Tyr Asp Leu Pro Pro Val Arg
 995 1000 1005

 His Pro Pro Ser Pro Pro Leu Arg Arg Gln Asp Arg
 1010 1015 1020

<210> 3
 <211> 2919

<212> DNA

<213> Homo sapiens

<400> 3

agatctctgc agacaggtcc tccaggctgc tggctgcagc gccactgccc actctgcgcc 60

ggtcttgctg caggcctctg caatgtcacc gcctctgtgt cccctccttc tcctggctgt 120
ggccctgcgg ctggctggaa ctctcaaccc cagtatccc aatacctgca gcttctggaa 180
aagtttcaact accaccacca aggagtcaca ctcccggccc ttcaagcctgc tcccctcaga 240
gccctgcgag cggccctggg agggccccc tacttgcggg cagcccacgg ttgtataccg 300
gaccgtgtac cgtcagggtgg tgaagacgga ccaccgcccag cgcctgcagt gctgccatgg 360
cttctatgag agcaggggggt tctgtgtccc gctctgtgcc caggagtgtg tccatggccg 420
ttgtgtggca cccaatcagt gccaatgtgt gccaggctgg cggggcgacg actgttccag 480
tgagtgtgcc ccagaatgt gggggccaca gtgtgacaag ccctgcagct gcggcaacaa 540
cagctgtgt gatcccaaga gtggggatgt ttcttgcct tctggctgc agccccccgaa 600
ctgccttcag ccctgtaccc ctggctacta tggccctgccc tgccagttcc gctgccagtg 660
ccatggggca ccctgcgatc cccagactgg agcctgcctc tgcccccgag agagaactgg 720
gcccagctgt gacgtgtctt gttcccaggg cacttctggc ttcttctgccc ccagcacccca 780
ttcttgccaa aatggaggtg tcttccaaac cccacaggc tcctgcagct gccccctgg 840
ctggatggta tggaggggtgg ggcctgtggg catgggtgt gggtctgggg agaattctgt 900
gggtgggtgct aagcagggtc ccaaggcgc acatctgcctc ctgcccctgccc cagagggctt 960
tcacggaccc aactgctccc aggaatgtcg ctggcacaac ggcggcctct gtgaccgatt 1020
caactggcag tgccgtcg ctcgggtta cactgggat cggtgccggg aggagtgcgg 1080
ggtgggccgc tttgggcagg actgtgtcga gacgtgcgcac tgcccccgg acgcccgtt 1140
cttcccgccc aacggcgcac gtctgtgcga acacggcttc actggggacc gctgcacgg 1200
tcgcctctgc cccgacggct tctacggctc cagctgcag qccccccgca cctgcgaccg 1260
ggagcacagc ctcaactgtcc acccgatgaa cggggagtgc tcctgcctgc cgggctggc 1320
gggcctccac tgcaacgaga gctgcccga ggacacgcac gggccagggt gccaggagca 1380
ctgtctctgc ctgcacgggtg gctgtgcga ggctaccagc ggctctgtc agtgcgcgccc 1440
gggttacacg ggcctcact gtgtacttct ttgtcctctt gacacctacg gtgtcaactg 1500
ttctgcacgc tgctcatgtg aaaatgcacat cgcctgcctca cccatcgacg gcgagtgcg 1560
ctgcaaggaa ggttggcgc gttgttaactg ctctgtgc tggccacccg gaacctgggg 1620
cttcagttgc aatgccagct gccagtgtgc ccatgaggca gtctgcagcc cccaaactgg 1680
agcctgtacc tgcaacccctg ggtggcatgg ggcccactgc cagctgcctt gtccgaagg 1740
gcagtttggaa gaaggttggc gcaactgc tgactgtgac cactctgatg gctgtgaccc 1800
tggtcatggaa cgctgtcactt gccaggctgg ctggatgggt gcccgtgcc acctgtctt 1860
ccctgaggc ttatggggag tcaactgttag caacacctgc acctgcaaga atgggggcac 1920
ctgtctccct gagaatggca actgcgtgtg tgcggccggaa ttccggggcc cttcctgcca 1980
gagatcctgt cagccgtggc gctatggca acgtgtgtg ccctgcaagt gcgctaacca 2040
ctccctctgc caccctcgaa acggggcctg ctactgcctg gctggctggaa caggccccga 2100
ctgctccctg ccatgcccctc caggacactg gggagaaaaac tggcccaaga cctgccaatg 2160
tcaccatgtt gggacctgccc atccccagga tggagactgt atctgccttcc taggctggac 2220
tggacaccac tgcttagaaag gctgcctctt gggacattt ggtgtcaact gctcccagcc 2280
atgcccgtgt ggtcctggag aaaagtgcac cccagagact gggccctgtg tatgtcccc 2340
agggcacagt ggtgcacccctt gcaggatgg aatccaggag cccttactg tgatgccgac 2400
caactccagta gcgtataact cgctgggtgc agtgattggc attgcagtgc tggggccctt 2460
tgtggtagcc ctggggcac tggtcatgtt ctatcgccac tggcaaaaag acaaggagca 2520
ccaccacccgt gctgtggctt acagcagcgg ggcctggac ggctccaggt atgtcatgccc 2580
agatgtccctt ccgagactaca gtcactacta ctccaacccc agtaccacaca ccctgtcgca 2640
gtgctccctt aaccccccac cccctaacaa ggttccaggc cgccttttgc ccagcctgca 2700
gaaccctgag cggccagggtg gggcccaagg gcatgataac cacaccaccc tgcctgctga 2760
ctggaaaggcac cgcggggagc cccctccagg gcctctggac agggtaggt gcccggaggc 2820
cagggtctt ggcgcgggtg gatgtgtgca gcccagatgc cgcgtctgag tggatgtgtc 2880
tggagacggg ggctctggc cccatttcta gaggaagtg 2919

<210> 4
<211> 928
<212> PRT
<213> Homo sapiens

<400> 4
Met Ser Pro Pro Leu Cys Pro Leu Leu Leu Leu Ala Val Gly Leu Arg
1 5 10 15
Leu Ala Gly Thr Leu Asn Pro Ser Asp Pro Asn Thr Cys Ser Phe Trp
20 25 30
Glu Ser Phe Thr Thr Thr Lys Glu Ser His Ser Arg Pro Phe Ser
35 40 45
Leu Leu Pro Ser Glu Pro Cys Glu Arg Pro Trp Glu Gly Pro His Thr
50 55 60
Cys Pro Gln Pro Thr Val Val Tyr Arg Thr Val Tyr Arg Gln Val Val
65 70 75 80
Lys Thr Asp His Arg Gln Arg Leu Gln Cys Cys His Gly Phe Tyr Glu
85 90 95
Ser Arg Gly Phe Cys Val Pro Leu Cys Ala Gln Glu Cys Val His Gly
100 105 110
Arg Cys Val Ala Pro Asn Gln Cys Gln Cys Val Pro Gly Trp Arg Gly
115 120 125
Asp Asp Cys Ser Ser Glu Cys Ala Pro Gly Met Trp Gly Pro Gln Cys
130 135 140
Asp Lys Pro Cys Ser Cys Gly Asn Asn Ser Ser Cys Asp Pro Lys Ser
145 150 155 160
Gly Val Cys Ser Cys Pro Ser Gly Leu Gln Pro Pro Asn Cys Leu Gln
165 170 175
Pro Cys Thr Pro Gly Tyr Tyr Gly Pro Ala Cys Gln Phe Arg Cys Gln
180 185 190
Cys His Gly Ala Pro Cys Asp Pro Gln Thr Gly Ala Cys Phe Cys Pro
195 200 205
Ala Glu Arg Thr Gly Pro Ser Cys Asp Val Ser Cys Ser Gln Gly Thr

210 215 220
Ser Gly Phe Phe Cys Pro Ser Thr His Ser Cys Gln Asn Gly Gly Val
225 230 235 240
Phe Gln Thr Pro Gln Gly Ser Cys Ser Cys Pro Pro Gly Trp Met Val
245 250 255
Trp Arg Val Gly Pro Val Gly Met Gly Cys Gly Ser Gly Glu Asn Ser
260 265 270
Val Gly Gly Ala Lys Gln Gly Ser Lys Gly Thr Ile Cys Ser Leu Pro
275 280 285
Cys Pro Glu Gly Phe His Gly Pro Asn Cys Ser Gln Glu Cys Arg Cys
290 295 300
His Asn Gly Gly Leu Cys Asp Arg Phe Thr Gly Gln Cys Arg Cys Ala
305 310 315 320
Pro Gly Tyr Thr Gly Asp Arg Cys Arg Glu Glu Cys Pro Val Gly Arg
325 330 335
Phe Gly Gln Asp Cys Ala Glu Thr Cys Asp Cys Ala Pro Asp Ala Arg
340 345 350
Cys Phe Pro Ala Asn Gly Ala Cys Leu Cys Glu His Gly Phe Thr Gly
355 360 365
Asp Arg Cys Thr Asp Arg Leu Cys Pro Asp Gly Phe Tyr Gly Leu Ser
370 375 380
Cys Gln Ala Pro Arg Thr Cys Asp Arg Glu His Ser Leu Ser Cys His
385 390 395 400
Pro Met Asn Gly Glu Cys Ser Cys Leu Pro Gly Trp Ala Gly Leu His
405 410 415
Cys Asn Glu Ser Cys Pro Gln Asp Thr His Gly Pro Gly Cys Gln Glu
420 425 430
His Cys Leu Cys Leu His Gly Gly Val Cys Gln Ala Thr Ser Gly Leu
435 440 445
Cys Gln Cys Ala Pro Gly Tyr Thr Gly Pro His Cys Ala Ser Leu Cys
450 455 460
Pro Pro Asp Thr Tyr Gly Val Asn Cys Ser Ala Arg Cys Ser Cys Glu

465	470	475	480
Asn Ala Ile Ala Cys Ser Pro Ile Asp Gly Glu Cys Val Cys Lys Glu			
485	490	495	
Gly Trp Gln Arg Gly Asn Cys Ser Val Pro Cys Pro Pro Gly Thr Trp			
500	505	510	
Gly Phe Ser Cys Asn Ala Ser Cys Gln Cys Ala His Glu Ala Val Cys			
515	520	525	
Ser Pro Gln Thr Gly Ala Cys Thr Cys Thr Pro Gly Trp His Gly Ala			
530	535	540	
His Cys Gln Leu Pro Cys Pro Lys Gly Gln Phe Gly Glu Gly Cys Ala			
545	550	555	560
Ser Arg Cys Asp Cys Asp His Ser Asp Gly Cys Asp Pro Val His Gly			
565	570	575	
Arg Cys Gln Cys Gln Ala Gly Trp Met Gly Ala Arg Cys His Leu Ser			
580	585	590	
Cys Pro Glu Gly Leu Trp Gly Val Asn Cys Ser Asn Thr Cys Thr Cys			
595	600	605	
Lys Asn Gly Gly Thr Cys Leu Pro Glu Asn Gly Asn Cys Val Cys Ala			
610	615	620	
Pro Gly Phe Arg Gly Pro Ser Cys Gln Arg Ser Cys Gln Pro Gly Arg			
625	630	635	640
Tyr Gly Lys Arg Cys Val Pro Cys Lys Cys Ala Asn His Ser Phe Cys			
645	650	655	
His Pro Ser Asn Gly Ala Cys Tyr Cys Leu Ala Gly Trp Thr Gly Pro			
660	665	670	
Asp Cys Ser Gln Pro Cys Pro Pro Gly His Trp Gly Glu Asn Cys Ala			
675	680	685	
Gln Thr Cys Gln Cys His His Gly Gly Thr Cys His Pro Gln Asp Gly			
690	695	700	
Ser Cys Ile Cys Pro Leu Gly Trp Thr Gly His His Cys Leu Glu Gly			
705	710	715	720
Cys Pro Leu Gly Thr Phe Gly Ala Asn Cys Ser Gln Pro Cys Gln Cys			

725	730	735
Gly Pro Gly Glu Lys Cys His Pro Glu Thr Gly Ala Cys Val Cys Pro		
740	745	750
Pro Gly His Ser Gly Ala Pro Cys Arg Ile Gly Ile Gln Glu Pro Phe		
755	760	765
Thr Val Met Pro Thr Thr Pro Val Ala Tyr Asn Ser Leu Gly Ala Val		
770	775	780
Ile Gly Ile Ala Val Leu Gly Ser Leu Val Val Ala Leu Val Ala Leu		
785	790	795
Phe Ile Gly Tyr Arg His Trp Gln Lys Asp Lys Glu His His His Leu		
805	810	815
Ala Val Ala Tyr Ser Ser Gly Arg Leu Asp Gly Ser Glu Tyr Val Met		
820	825	830
Pro Asp Val Pro Pro Ser Tyr Ser His Tyr Tyr Ser Asn Pro Ser Tyr		
835	840	845
His Thr Leu Ser Gln Cys Ser Pro Asn Pro Pro Pro Asn Lys Val		
850	855	860
Pro Gly Pro Leu Phe Ala Ser Leu Gln Asn Pro Glu Arg Pro Gly Gly		
865	870	875
880		
Ala Gln Gly His Asp Asn His Thr Thr Leu Pro Ala Asp Trp Lys His		
885	890	895
Arg Arg Glu Pro Pro Pro Gly Pro Leu Asp Arg Gly Arg Cys Arg Glu		
900	905	910
Ala Arg Val Ser Gly Ala Gly Gly Cys Val Gln Pro Arg Cys Arg Val		
915	920	925

<210> 5
<211> 2919
<212> DNA
<213> Homo sapiens

<400> 5

agatctctgc agacaggctcc tccaggctgc tggctgcagc gccactgccc actctgcgcc 60
gttcttgcgtc caggcctctg caatgtcacc gcctctgtgt cccctccctc tcctggctgt 120
gggcctgcgg ctggctggaa ctctcaaccc cagtatccc aatacctgca gcttctggaa 180
aagcttcaact accaccacca aggagtccca ctcccggccc ttcagcctgc tcccctcaga 240
gccctgcgag cggccctggg agggccccc tacttgcggc cagccacgg ttgtataccg 300
gaccgtgtac cgtcaggtgg tgaagacgga ccaccgcag cgcctgcagt gctgccatgg 360
cttctatgag agcaggggggt tctgtgtccc gctctgtgcc caggagtgtg tccatggccg 420
ttgtgtggca cccaatcagt gccaatgtgt gccaggctgg cggggcgacg actgttccag 480
tgagtgtgcc ccaggaatgt gggggccaca gtgtgacaag ccctgcagct gcccgaacaa 540
cagctcgtgt gatcccaaga gtggggatgt ttcttgcctc tctggctgc agccccccgaa 600
ctgccttcaag ccctgttaccc ctggctacta tggccctgccc tgccagttcc gctgccagtg 660
ccatggggca ccctgcgtc cccagactgg agcctgcgtc tgcccccgcag agagaactgg 720
gcccagctgt gacgtgtcct gttcccaggg cacttctggc ttcttctgccc ccagcacccca 780
ttcttgccaa aatggaggtg tcttccaaac cccacagggc tcctgcagct gccccctgg 840
ctggatggta tggaggggtgg ggcctgtggg catgggggtgt gggcttggg agaattctgt 900
gggtgggtgt aagcagggct ccaagggcac catctgcgtcc ctgcctgccc cagagggcctt 960
tcacggaccc aactgctccc aggaatgtcg ctgccacaac ggcggccctc gtgaccgatt 1020
caactggcag tgccgctgcg ctccgggtta cactggggat cggtgccggg aggagtgc 1080
ggtggccgc tttgggcagg actgtgtcga gacgtgcgac tgccggccgg acgcccgtt 1140
cttccggcc aacggcgcac gtctgtgcga acacggcttc actggggacc gctgcacgg 1200
tcgcctctgc cccgacggct tctacggct cagctgcagc gccccccca cctgcgaccg 1260
ggagcacacg ctcaagctgc acccgatgaa cggggagtgc tcctgcctgc cgggcttggc 1320
gggcctccac tgcaacgaga gctgcccgcg ggacacgcac gggccagggt gccaggagcg 1380
ctgtctctgc ctgcacgggt ggcgtctgcca ggctaccagc ggcctctgtc agtgcgcg 1440
gggttacacg ggcctctact gtgcttagtct ttgtcctctc gacacctacg gtgtcaactg 1500
ttctgcacgc tgctcatgtg aaaatgcacat cgctgcgtca cccatgcacg gcgagtgccgt 1560
ctgcaaggaa ggttggcagc gtggtaactg ctctgtgc tggccaccccg gaaccttggg 1620
cttcagttgc aatgccagct gccagtgtgc ccatgaggca gtctgcagcc cccaaactgg 1680
agcctgtacc tgacccctg ggtggcatgg ggcccactgc cagctccct gtcggaaagg 1740
gcagtttggaa gaaggttggc ccagtcgtc tgactgtgac cactctgtatg gctgtgaccc 1800
tggtcatggaa cgctgtcagt gccaggctgg ctggatgggt gcccgtgcc acctgtcctg 1860
ccctgagggc ttatggggag tcaactgttag caacacctgc acctgcaaga atgggggcac 1920
ctgtctccct gagaatggca actgcgtgt tgccggccga ttccggggcc cctcctgcca 1980
gagatccctg cagcctggcc gctatggcaa acgctgtgtg ccctgcaagt ggcctaacc 2040
ctccttctgc caccctcga acggggcctg ctactgcctg gctggctgga caggcccccga 2100
ctgctccctc ccatgcctc caggacactg gggagaaaac tggcccaga cctgccaatg 2160
tcaccatgtt gggacctgccc atccccagga tggagactgt atctgccttcc taggctggac 2220
tggacaccac tgcttagaaag gctgcccctt gggagacattt ggtgctact gctcccagcc 2280
atgccagttgt ggtcctggag aaaagtgcac cccagagact gggccctgtg tatgtcccc 2340
agggcacagt ggtgcacccct gcaggattgg aatccaggag cccttactg tgatgccgac 2400
caactccagta gcgtataact cgctgggtgc agtattggc attgcagtgc tggggccct 2460
tgtggtagcc ctggtggcac tggctatgg ctatcgac tggcaaaaag acaaggagca 2520
ccaccacctg gctgtggctt acagcagcgg gcgcctggac ggctccgagt atgtcatgcc 2580
agatgtccct ccgagctaca gtcactacta ctccaacccc agtaccaca ccctgtcgca 2640
gtgctccctt aaccctccac cccctaacaa ggttccaggg cgcgtctttt ccagcctgca 2700
gaaccctgag cggccaggtg gggcccaagg gcatgataac cacaccaccc tgccctgctga 2760
ctggaaagcac cgccgggagc cccctccagg gcctctggac agggtaggt gccgggaggc 2820
cagggtctt ggcgcgggtg gatgtgtgca gcccagatgc cgcgtctgag tttgtgtgtc 2880

tggagacggg ggctctggc cccatttcta gaggaagtg

2919

<210> 6
<211> 928
<212> PRT
<213> Homo sapiens

<400> 6
Met Ser Pro Pro Leu Cys Pro Leu Leu Leu Ala Val Gly Leu Arg
1 5 10 15

Leu Ala Gly Thr Leu Asn Pro Ser Asp Pro Asn Thr Cys Ser Phe Trp
20 25 30

Glu Ser Phe Thr Thr Thr Lys Glu Ser His Ser Arg Pro Phe Ser
35 40 45

Leu Leu Pro Ser Glu Pro Cys Glu Arg Pro Trp Glu Gly Pro His Thr
50 55 60

Cys Pro Gln Pro Thr Val Val Tyr Arg Thr Val Tyr Arg Gln Val Val
65 70 75 80

Lys Thr Asp His Arg Gln Arg Leu Gln Cys Cys His Gly Phe Tyr Glu
85 90 95

Ser Arg Gly Phe Cys Val Pro Leu Cys Ala Gln Glu Cys Val His Gly
100 105 110

Arg Cys Val Ala Pro Asn Gln Cys Gln Cys Val Pro Gly Trp Arg Gly
115 120 125

Asp Asp Cys Ser Ser Glu Cys Ala Pro Gly Met Trp Gly Pro Gln Cys
130 135 140

Asp Lys Pro Cys Ser Cys Gly Asn Asn Ser Ser Cys Asp Pro Lys Ser
145 150 155 160

Gly Val Cys Ser Cys Pro Ser Gly Leu Gln Pro Pro Asn Cys Leu Gln
165 170 175

Pro Cys Thr Pro Gly Tyr Gly Pro Ala Cys Gln Phe Arg Cys Gln
180 185 190

Cys His Gly Ala Pro Cys Asp Pro Gln Thr Gly Ala Cys Phe Cys Pro
195 200 205

Ala Glu Arg Thr Gly Pro Ser Cys Asp Val Ser Cys Ser Gln Gly Thr
210 215 220

Ser Gly Phe Phe Cys Pro Ser Thr His Ser Cys Gln Asn Gly Gly Val
225 230 235 240

Phe Gln Thr Pro Gln Gly Ser Cys Ser Cys Pro Pro Gly Trp Met Val
245 250 255

Trp Arg Val Gly Pro Val Gly Met Gly Cys Gly Ser Gly Glu Asn Ser
260 265 270

Val Gly Gly Ala Lys Gln Gly Ser Lys Gly Thr Ile Cys Ser Leu Pro
275 280 285

Cys Pro Glu Gly Phe His Gly Pro Asn Cys Ser Gln Glu Cys Arg Cys
290 295 300

His Asn Gly Gly Leu Cys Asp Arg Phe Thr Gly Gln Cys Arg Cys Ala
305 310 315 320

Pro Gly Tyr Thr Gly Asp Arg Cys Arg Glu Glu Cys Pro Val Gly Arg
325 330 335

Phe Gly Gln Asp Cys Ala Glu Thr Cys Asp Cys Ala Pro Asp Ala Arg
340 345 350

Cys Phe Pro Ala Asn Gly Ala Cys Leu Cys Glu His Gly Phe Thr Gly
355 360 365

Asp Arg Cys Thr Asp Arg Leu Cys Pro Asp Gly Phe Tyr Gly Leu Ser
370 375 380

Cys Gln Ala Pro Arg Thr Cys Asp Arg Glu His Ser Leu Ser Cys His
385 390 395 400

Pro Met Asn Gly Glu Cys Ser Cys Leu Pro Gly Trp Ala Gly Leu His
405 410 415

Cys Asn Glu Ser Cys Pro Gln Asp Thr His Gly Pro Gly Cys Gln Glu
420 425 430

Arg Cys Leu Cys Leu His Gly Gly Val Cys Gln Ala Thr Ser Gly Leu
435 440 445

Cys Gln Cys Ala Pro Gly Tyr Thr Gly Pro His Cys Ala Ser Leu Cys
450 455 460

Pro Pro Asp Thr Tyr Gly Val Asn Cys Ser Ala Arg Cys Ser Cys Glu
465 470 475 480

Asn Ala Ile Ala Cys Ser Pro Ile Asp Gly Glu Cys Val Cys Lys Glu
485 490 495

Gly Trp Gln Arg Gly Asn Cys Ser Val Pro Cys Pro Pro Gly Thr Trp
500 505 510

Gly Phe Ser Cys Asn Ala Ser Cys Gln Cys Ala His Glu Ala Val Cys
515 520 525

Ser Pro Gln Thr Gly Ala Cys Thr Cys Thr Pro Gly Trp His Gly Ala
530 535 540

His Cys Gln Leu Pro Cys Pro Lys Gly Gln Phe Gly Glu Gly Cys Ala
545 550 555 560

Ser Arg Cys Asp Cys Asp His Ser Asp Gly Cys Asp Pro Val His Gly
565 570 575

Arg Cys Gln Cys Gln Ala Gly Trp Met Gly Ala Arg Cys His Leu Ser
580 585 590

Cys Pro Glu Gly Leu Trp Gly Val Asn Cys Ser Asn Thr Cys Thr Cys
595 600 605

Lys Asn Gly Gly Thr Cys Leu Pro Glu Asn Gly Asn Cys Val Cys Ala
610 615 620

Pro Gly Phe Arg Gly Pro Ser Cys Gln Arg Ser Cys Gln Pro Gly Arg
625 630 635 640

Tyr Gly Lys Arg Cys Val Pro Cys Lys Cys Ala Asn His Ser Phe Cys
645 650 655

His Pro Ser Asn Gly Ala Cys Tyr Cys Leu Ala Gly Trp Thr Gly Pro
660 665 670

Asp Cys Ser Gln Pro Cys Pro Pro Gly His Trp Gly Glu Asn Cys Ala
675 680 685

Gln Thr Cys Gln Cys His His Gly Gly Thr Cys His Pro Gln Asp Gly
690 695 700

Ser Cys Ile Cys Pro Leu Gly Trp Thr Gly His His Cys Leu Glu Gly
705 710 715 720

Cys Pro Leu Gly Thr Phe Gly Ala Asn Cys Ser Gln Pro Cys Gln Cys
725 730 735

Gly Pro Gly Glu Lys Cys His Pro Glu Thr Gly Ala Cys Val Cys Pro
740 745 750

Pro Gly His Ser Gly Ala Pro Cys Arg Ile Gly Ile Gln Glu Pro Phe
755 760 765

Thr Val Met Pro Thr Pro Val Ala Tyr Asn Ser Leu Gly Ala Val
770 775 780

Ile Gly Ile Ala Val Leu Gly Ser Leu Val Val Ala Leu Val Ala Leu
785 790 795 800

Phe Ile Gly Tyr Arg His Trp Gln Lys Asp Lys Glu His His His Leu
805 810 815

Ala Val Ala Tyr Ser Ser Gly Arg Leu Asp Gly Ser Glu Tyr Val Met
820 825 830

Pro Asp Val Pro Pro Ser Tyr Ser His Tyr Tyr Ser Asn Pro Ser Tyr
835 840 845

His Thr Leu Ser Gln Cys Ser Pro Asn Pro Pro Pro Asn Lys Val
850 855 860

Pro Gly Pro Leu Phe Ala Ser Leu Gln Asn Pro Glu Arg Pro Gly Gly
865 870 875 880

Ala Gln Gly His Asp Asn His Thr Thr Leu Pro Ala Asp Trp Lys His
885 890 895

Arg Arg Glu Pro Pro Pro Gly Pro Leu Asp Arg Gly Arg Cys Arg Glu
900 905 910

Ala Arg Val Ser Gly Ala Gly Gly Cys Val Gln Pro Arg Cys Arg Val
915 920 925

<210> 7
<211> 5000
<212> DNA
<213> Homo sapiens

<400> 7

agatctctgc agacagggtcc tccagggtgc tggctgcagc gccactgccc actctgcgcc 60
ggtcttgctg caggcctctg caatgtcacc gcctctgtgt cccctcccttc tcctggctgt 120
gggcctgcgg ctggctggaa ctctcaaccc cagtatccc aataacctgca gcttctggaa 180
aagcttcaact accaccacca aggagtcacc ccccccccccc ttcagcctgc tcccctcaga 240
gccctgcgag cgcccctggg agggccccca tacttgcccc cagccacgg ttgtataccg 300
gaccgtgtac cgtcagggtgg tgaagacgga coaccgccag cgccctgcagt gtcgcctagg 360
cttctatgag agcaggggggt tctgtgtccc gctctgtgcc caggagtgtg tccatggccg 420
ttgtgtggca cccaatcagt gccaatgtgt gcaggcgtgg cggggcgacg actgttccag 480
tgagtgtgcc ccaggaatgt gggggccaca gtgtgacaag ccctgcagct gcgcaacaa 540
cagctcggt gatcccaaga gtgggtatg ttcttgccct tctggctgc agccccccgaa 600
ctgccttcag ccctgtaccc ctggctacta tggccctgccc tgccagttcc gtcgcctagg 660
ccatggggca ccctgcgatc cccagactgg agcctgccttc tgcccccag agagaactgg 720
gcccagctgt gacgtgtcct gttcccaggg cacttctggc ttcttctgcc ccagcaccca 780
tccttgccaa aatggagggtg tcttccaaac cccacagggc tcctgcagct gccccccctgg 840
ctggatggc accatctgct ccctgcctg cccagagggc ttacacggac ccaactgctc 900
ccaggaatgt cgctgcccaca acggcggtt ctgtgaccga ttacacggc agtgcgcgtg 960
cgctccgggt tacactgggg atcgggtgccg ggaggagtgc cgggtggcc gcttggcga 1020
ggactgtgct gagacgtgctg actgcgcccc ggacgcccgt tgcttcccg ccaacggcgc 1080
atgtctgtgc gaacacggct tcaactggga cggctgcacg gatgcctct gccccgacgg 1140
cttctacggc ctcagctgcc aggccccccg cacctgcgac cgggagcaca gcctcagctg 1200
ccacccatg aacggggagt gtcctgcct gccgggctgg gccccctcc actgcaacaca 1260
gagctgccc caggacacgc atggggcagg gtgccaggag cactgtctct gcctgcacgg 1320
tggcgctgc caggctacca gcggcctctg tcaactgcgcg cgggttaca cggccctca 1380
ctgtgctagt ctttgcctc ctgacaccta cgggtcaac tggctgcac gtcgtcatg 1440
tgaaaatgcc atcgcctgct caccatcga cggcgagtgc gtctgcaagg aagggttggca 1500
gcgtggtaac tgctctgtgc cctgcccacc cggAACCTGG ggcttcagtt gcaatggcag 1560
ctgccagtgt gcccattgagg cagtctgcag cccccaact ggacgctgta cctgcacccc 1620
tgggtggcat gggggccact gccagctgcc ctgtccgaaagg gggcagttt gagaaggttg 1680
tgccagtcgc tggactgtg accactctga tggctgtac cctgttcatg gacgctgtca 1740
gtgccaggct ggctggatgg gtgcccctg ccacctgtcc tgccctgagg gcttatgggg 1800
agtcaactgt agcaacaccc gcacctgcaaa gaatgggggc acctgtctcc ctgagaatgg 1860
caactgcgtg tggcgcccc gattccgggg cccctcctgc cagagatctt gtcagcctgg 1920
ccgctatggc aaacgctgtg tgccctgcaaa gtgcgctaaac cactcctct gccacccctc 1980
gaacgggacc tgctactgcc tggctggctg gacaggcccc gactgtccc agccatgccc 2040
tccaggacac tggggagaaa actgtgccc gacctgccaa tgtcaccatg gtgggacctg 2100
ccatccccag gatgggagct gatctgcctt cctaggctgg actggacacc actgcttaga 2160
aggctccct ctggggacat ttgggtctaa ctgctccctg ccatgccagt gtggctctgg 2220
agaaaagtgc caccctgaga ctggggctg tggatgtccc ccagggcaca gtgggtgcacc 2280
ttgcaggatt ggaatccagg agccctttac tggatgtccg accactccag tagcgtataa 2340
ctcgctgggt gcagtgattt gcattgcagt gctggggctt cttgtggtag ccctgggtggc 2400
actgttccatt ggatctggc actggcaaaa agacaaggag caccaccacc tggctgtggc 2460
ttacagcagc gggcgctgg acggctccga gtatgtcatg ccagatgtcc ctccgagct 2520
cagtcactac tactccaacc ccagctacca caccctgtcg cagtgtccc caaaccctcc 2580
accccttaac aaggttccag gcccgtctt tgccagctgg cagaaccctg agcggccagg 2640
tggggcccaa gggcatgata accacaccac cctgcctgt gactgaaagc accgcccggg 2700
gccccctcca gggcctctgg acagggggag cagccgcctg gaccgaagct acagctata 2760
ctacagcaat gggccaggcc cattctacaa taaagggtctt atctctgaag aggagctctg 2820

ggccagtgtg gcttccctga gcagtgagaa cccatatgcc accatccggg acctgcccag 2880
 cttgccagg ggccccggg agagcagta catggagatg aaaggccctc cctcaggatc 2940
 tccccccagg cagcctcctc agttctggta cagccagagg cggcggcaac cccagccaca 3000
 gagagacagt ggcacctacg agcagcccg cccctgatc catgaccgag actctgtggg 3060
 ctcccagccc cctctgcctc cgggcctacc cccggccac tatgactcac ccaagaacag 3120
 ccacatccct ggacattatg acttgcctcc agtacggcat ccccatcac ctccacttcg 3180
 acgcccaggac cggttggagg ccaggatgtt atggcagagg ccagcacacc tggctgtgc 3240
 tgctcaaggc tggggacaga gcctagtgtc cccctgcccag gagcaggag tggaccggca 3300
 ggctgtgaac atgaacaacg cttAACAGAG caagtgtatgg gagcctgtt cctgggtct 3360
 accatgggag acgctgatca gcaggatgtcc tggctccctt tcccaaccca ctgctcccaa 3420
 ggcctccagg gcccgtgtc cataaaactgg tgggtggaa gttgctgggt aactctgtt 3480
 tcagacatgc gtgtgggtt cctttctgt gcatgctcag cctgggtct gtgcgtgtgt 3540
 gtgtttctgt gatttttagaa gggttaccagg cacaggttct gtccttagggc attaccatt 3600
 tagtagggag atgaaaccaa cccaattaac tctagcaata gcctcctaac tggcctcctc 3660
 cattgattca gtgaaccttc caatgcatttgc ctcatataattt caaaatacag gctggtagt 3720
 tactccctac ctgaaaggctt tcataagggtc ctcttgctc ttctgcccagt atcaaaactt 3780
 ttgaaggcct taaaggccct gctttgcctg gcccattctgt ctctccagcc tcacccctgaa 3840
 ctgtgttcct gtcactgcac gccagtcaca ccggcctcta ggtcctcctg taggcccactc 3900
 ttctttctgg cacagggacc tgcacacctg gagtgcctt cctcccccac tcgcctgttc 3960
 accccctgctt ttcccttaca cctccctcctc agggaaatgc ccaccctccg tacatcttc 4020
 acagccctga ttgcagctgt gttcactcac cagttacctg cagaaggcct acagggtgcc 4080
 aggcaacttct ttaatgggtt ctttctttat gtgattattt gattaatctc tgcctccccc 4140
 actagactgt aagctccctg aaggcaagaa tcctgtgtt atgctcaata ttagctctcc 4200
 cttggcacag agtaggcact caacaaatgc tccccaaaag gctgagtgcc tgactgaatt 4260
 aagtaccagt gacatgcagt aactgctaaatg atagatgagc catctgtatg ctctgacagt 4320
 tacagactga ataagttggta gacttcctta aagggtggca tttcccccagg gtaacaacgc 4380
 agagctcagg tgtggaaagg tgccaggggc aggggtgcag aggggctgag gctgaggggg 4440
 gtgcagggc tggagaaagg ataacaggag agagtataca ggcattgcctt gatttattgc 4500
 acttcacagg tagcagaatt tttaaagaaaa ttgaagggtt tggacatata atgtgacagc 4560
 aataggttaa gaaaagcaaa gcagagaaat tgaagatttg tgtcaacact gcttaagca 4620
 aatctgttgg caccattttt ccaatagcat gtgccttattt tgggtctcta cattgcattt 4680
 tggtaattgc ttgcaatatt tcaagcattt tcattgttat tatatgtgtt atagtgtatct 4740
 gtgatcagt atcttgata tattattgtt attgtttcg ggcgcattga accgcaccca 4800
 tataacacgg taaacttaat cagcaaaaaa aaaaaaaaaa aaaaaacccg gaaaaatttt 4860
 agaattgaaa aatatgaaaa acccccgggg gggcttttc aggggggggc gggccccca 4920
 atttaaattt tttttttttt aacaaggta agtccctttt ttgagaaaaa aatcctcctg 4980
 aaagattaaa tttggggggcc 5000

<210> 8
 <211> 1037
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ser Pro Pro Leu Cys Pro Leu Leu Leu Ala Val Gly Leu Arg
 1 5 10 15

Leu Ala Gly Thr Leu Asn Pro Ser Asp Pro Asn Thr Cys Ser Phe Trp
20 25 30

Glu Ser Phe Thr Thr Thr Lys Glu Ser His Ser Arg Pro Phe Ser
35 40 45

Leu Leu Pro Ser Glu Pro Cys Glu Arg Pro Trp Glu Gly Pro His Thr
50 55 60

Cys Pro Gln Pro Thr Val Val Tyr Arg Thr Val Tyr Arg Gln Val Val
65 70 75 80

Lys Thr Asp His Arg Gln Arg Leu Gln Cys Cys His Gly Phe Tyr Glu
85 90 95

Ser Arg Gly Phe Cys Val Pro Leu Cys Ala Gln Glu Cys Val His Gly
100 105 110

Arg Cys Val Ala Pro Asn Gln Cys Gln Cys Val Pro Gly Trp Arg Gly
115 120 125

Asp Asp Cys Ser Ser Glu Cys Ala Pro Gly Met Trp Gly Pro Gln Cys
130 135 140

Asp Lys Pro Cys Ser Cys Gly Asn Asn Ser Ser Cys Asp Pro Lys Ser
145 150 155 160

Gly Val Cys Ser Cys Pro Ser Gly Leu Gln Pro Pro Asn Cys Leu Gln
165 170 175

Pro Cys Thr Pro Gly Tyr Gly Pro Ala Cys Gln Phe Arg Cys Gln
180 185 190

Cys His Gly Ala Pro Cys Asp Pro Gln Thr Gly Ala Cys Phe Cys Pro
195 200 205

Ala Glu Arg Thr Gly Pro Ser Cys Asp Val Ser Cys Ser Gln Gly Thr
210 215 220

Ser Gly Phe Phe Cys Pro Ser Thr His Pro Cys Gln Asn Gly Gly Val
225 230 235 240

Phe Gln Thr Pro Gln Gly Ser Cys Ser Cys Pro Pro Gly Trp Met Gly
245 250 255

Thr Ile Cys Ser Leu Pro Cys Pro Glu Gly Phe His Gly Pro Asn Cys
260 265 270

Ser Gln Glu Cys Arg Cys His Asn Gly Gly Leu Cys Asp Arg Phe Thr
275 280 285

Gly Gln Cys Arg Cys Ala Pro Gly Tyr Thr Gly Asp Arg Cys Arg Glu
290 295 300

Glu Cys Pro Val Gly Arg Phe Gly Gln Asp Cys Ala Glu Thr Cys Asp
305 310 315 320

Cys Ala Pro Asp Ala Arg Cys Phe Pro Ala Asn Gly Ala Cys Leu Cys
325 330 335

Glu His Gly Phe Thr Gly Asp Arg Cys Thr Asp Arg Leu Cys Pro Asp
340 345 350

Gly Phe Tyr Gly Leu Ser Cys Gln Ala Pro Arg Thr Cys Asp Arg Glu
355 360 365

His Ser Leu Ser Cys His Pro Met Asn Gly Glu Cys Ser Cys Leu Pro
370 375 380

Gly Trp Ala Gly Leu His Cys Asn Glu Ser Cys Pro Gln Asp Thr His
385 390 395 400

Gly Pro Gly Cys Gln Glu His Cys Leu Cys Leu His Gly Gly Val Cys
405 410 415

Gln Ala Thr Ser Gly Leu Cys Gln Cys Ala Pro Gly Tyr Thr Gly Pro
420 425 430

His Cys Ala Ser Leu Cys Pro Pro Asp Thr Tyr Gly Val Asn Cys Ser
435 440 445

Ala Arg Cys Ser Cys Glu Asn Ala Ile Ala Cys Ser Pro Ile Asp Gly
450 455 460

Glu Cys Val Cys Lys Glu Gly Trp Gln Arg Gly Asn Cys Ser Val Pro
465 470 475 480

Cys Pro Pro Gly Thr Trp Gly Phe Ser Cys Asn Ala Ser Cys Gln Cys
485 490 495

Ala His Glu Ala Val Cys Ser Pro Gln Thr Gly Ala Cys Thr Cys Thr
500 505 510

Pro Gly Trp His Gly Ala His Cys Gln Leu Pro Cys Pro Lys Gly Gln
515 520 525

Phe Gly Glu Gly Cys Ala Ser Arg Cys Asp Cys Asp His Ser Asp Gly
530 535 540

Cys Asp Pro Val His Gly Arg Cys Gln Cys Gln Ala Gly Trp Met Gly
545 550 555 560

Ala Arg Cys His Leu Ser Cys Pro Glu Gly Leu Trp Gly Val Asn Cys
565 570 575

Ser Asn Thr Cys Thr Cys Lys Asn Gly Gly Thr Cys Leu Pro Glu Asn
580 585 590

Gly Asn Cys Val Cys Ala Pro Gly Phe Arg Gly Pro Ser Cys Gln Arg
595 600 605

Ser Cys Gln Pro Gly Arg Tyr Gly Lys Arg Cys Val Pro Cys Lys Cys
610 615 620

Ala Asn His Ser Phe Cys His Pro Ser Asn Gly Thr Cys Tyr Cys Leu
625 630 635 640

Ala Gly Trp Thr Gly Pro Asp Cys Ser Gln Pro Cys Pro Pro Gly His
645 650 655

Trp Gly Glu Asn Cys Ala Gln Thr Cys Gln Cys His His Gly Gly Thr
660 665 670

Cys His Pro Gln Asp Gly Ser Cys Ile Cys Pro Leu Gly Trp Thr Gly
675 680 685

His His Cys Leu Glu Gly Cys Pro Leu Gly Thr Phe Gly Ala Asn Cys
690 695 700

Ser Gln Pro Cys Gln Cys Gly Pro Gly Glu Lys Cys His Pro Glu Thr
705 710 715 720

Gly Ala Cys Val Cys Pro Pro Gly His Ser Gly Ala Pro Cys Arg Ile
725 730 735

Gly Ile Gln Glu Pro Phe Thr Val Met Pro Thr Thr Pro Val Ala Tyr
740 745 750

Asn Ser Leu Gly Ala Val Ile Gly Ile Ala Val Leu Gly Ser Leu Val
755 760 765

Val Ala Leu Val Ala Leu Phe Ile Gly Tyr Arg His Trp Gln Lys Asp
770 775 780

Lys Glu His His His Leu Ala Val Ala Tyr Ser Ser Gly Arg Leu Asp
785 790 795 800

Gly Ser Glu Tyr Val Met Pro Asp Val Pro Pro Ser Tyr Ser His Tyr
805 810 815

Tyr Ser Asn Pro Ser Tyr His Thr Leu Ser Gln Cys Ser Pro Asn Pro
820 825 830

Pro Pro Pro Asn Lys Val Pro Gly Pro Leu Phe Ala Ser Leu Gln Asn
835 840 845

Pro Glu Arg Pro Gly Gly Ala Gln Gly His Asp Asn His Thr Thr Leu
850 855 860

Pro Ala Asp Trp Lys His Arg Arg Glu Pro Pro Pro Gly Pro Leu Asp
865 870 875 880

Arg Gly Ser Ser Arg Leu Asp Arg Ser Tyr Ser Tyr Ser Tyr Ser Asn
885 890 895

Gly Pro Gly Pro Phe Tyr Asn Lys Gly Leu Ile Ser Glu Glu Leu
900 905 910

Trp Ala Ser Val Ala Ser Leu Ser Ser Glu Asn Pro Tyr Ala Thr Ile
915 920 925

Arg Asp Leu Pro Ser Leu Pro Gly Gly Pro Arg Glu Ser Ser Tyr Met
930 935 940

Glu Met Lys Gly Pro Pro Ser Gly Ser Pro Pro Arg Gln Pro Pro Gln
945 950 955 960

Phe Trp Asp Ser Gln Arg Arg Arg Gln Pro Gln Pro Gln Arg Asp Ser
965 970 975

Gly Thr Tyr Glu Gln Pro Ser Pro Leu Ile His Asp Arg Asp Ser Val
980 985 990

Gly Ser Gln Pro Pro Leu Pro Pro Gly Leu Pro Pro Gly His Tyr Asp
995 1000 1005

Ser Pro Lys Asn Ser His Ile Pro Gly His Tyr Asp Leu Pro Pro Val
1010 1015 1020

Arg His Pro Pro Ser Pro Pro Leu Arg Arg Gln Asp Arg
1025 1030 1035

<210> 9
<211> 3114
<212> DNA
<213> Homo sapiens

<400> 9
atgtcaccgc ctctgtgtcc ctccttctc ctggctgtgg gcctgcggct ggctggaact 60
ctcaacccca gtatcccaa tacctgcagc ttctggaaa gcttcaactac caccaccaag 120
gagtcccaact cccccccctt cagcctgctc ccctcagagc cctgcgagcg gcccctggag 180
ggcccccata cttggccca gcccacggtt gtataccga ccgtgtaccg tcaggtggtg 240
aagacggacc accggcagcg cctgcagtgc tgccatggct tctatgagag cagggagttc 300
tgtgtcccgc tctgtgccc gggatgtgtc catggccgtt gtgtggcacc caatcagtgc 360
caatgtgtgc caggtggcg gggcgacgac tgttccagtg agtgtgcacc aggaatgtgg 420
gggccacagt gtgacaagcc ctgcagttgc ggcaacaaca gctcgtgtga tcccaagagt 480
ggggtatgtt cttggccctc tggtctgcag cccccaact gccttcagcc ctgtacccct 540
ggctactatg gcccgcctg ccagttccgc tgccagtgcc atggggcacc ctgcgatccc 600
cagactggag cctgcttctg ccccgacagag agaactgggc ccagctgtga cgtgtcctgt 660
tcccaggcga cttctggcctt cttctgcccc agcaccatc cttgcacaaa tggaggtgtc 720
ttccaaaccc cacagggctc ctgcagctgc cccctggct ggatgggcac catctgctcc 780
ctgcccgtcc cagagggcctt tcacggaccc aactgctccc aggaatgtcg ctgccacaac 840
ggcggccctt gtgaccgatt cactggcag tgccgctgc ctccgggta cactgggat 900
cggtgcccgg aggagtgtccc ggtggccgc tttggcagg actgtgtga gacgtgcgac 960
tgcgccccgg acgcccgtt cttccggcc aacggcgcatt gtctgtgcga acacggctt 1020
actggggacc gctgcacgga tcgcctctgc cccgacggct tctacggtct cagctgccag 1080
gccccctgca cctgcgaccg ggagcacacg ctcagctgca acccgatgaa cggggagtgc 1140
tcctgcctgc cgggctggc gggcctccac tgcaacgaga gctgcccga ggacacgcatt 1200
ggccaggggt gccaggagta ctgtctctgc ctgcacgggt gcgtctgcca ggctaccagc 1260
ggcctctgtc agtgcgcgccc gggttacacg ggcctcaact gtgctagtct ttgtcctcct 1320
gacacctacg gtgtcaactg ttctgcacgc tgctcatgtg aaaatgcatt cgcctgctca 1380
cccatcgacg gcgagtgcgt ctgcaaggaa ggttggcagc gtggtaactg ctctgtgccc 1440
tgccccacccg gaacctggg cttcagttgc aatgccagct gccagtgac ccatgaggca 1500
gtctgcagcc cccaaactgg agcctgtacc tgccatgtt ggtggcatgg ggcccactgc 1560
cagctccct gtccgaaggg gcagtttggaa gaaggttgg ccagtcgtt tgactgtgac 1620
caactgtatg gctgtgaccc ttttcattggaa cgctgtcaatg gccaggctgg ctggatgggt 1680
ggccgctgcc acctgtcctg ccctgaggc ttatggggag tcaactgttag caacacctgc 1740
acctgcaaga atggggcacc ctgtctccct gagaatggca actgcgtgtg tgccatggca 1800
ttccggggcc ctcctgcca gagatctgt cagcctggcc gctatggcaaa acgctgtgt 1860
ccctgcaagt gcgctaaccctt ctccctctgc caccctcgat acgggacactg ctactgcctg 1920
gctggctgga caggccccga ctgcctccatg ccatgcctc caggacactg gggagaaaaac 1980
tgtgcccaga cctgcaatgt tcaccatgtt gggacctgca atccccagga tggaggtgt 2040
atctgcccccc taggtggac tggacaccac tgcttagaaag gctgcctctt gggacattt 2100
ggtgctaact gctcccagcc atgcccgtgt ggtcctggag aaaagtgcac cccagagact 2160
ggggcctgtt tatgtcccccc agggcactgtt ggtgcaccc ttgcaggattgg aatccaggag 2220
ccctttactg tgatgcccac cactccatgt gctataact cgctgggtgc agtgattggc 2280
attgcagtgc tggggccct tgggttagcc ctggggcacc tggatggcattt ctatcggcacc 2340
tggcaaaaaag gcaaggagca ccaccacccg gctgtggctt acagcagcgg ggcgcctggac 2400
ggctccgagt atgtcatgca agatgtccct ccgagctaca gtcactacta ctccaaaccc 2460

agctaccaca ccctgtcgca gtgctccca aaccccccac cccctaacaa ggttccaggc 2520
ccgctcttg ccagcctgca gaaccctgag cggccaggtg gggcccaagg gcatgataac 2580
cacaccaccc tgcctgctga ctggaagcac cgccggagc cccctccagg gcctctggac 2640
agggggagca gccacctgga ccgaagctac agctatagct acagcaatgg cccaggccca 2700
ttctacgata aagggctcat ctctgaagag gagctgggg ccagtgtgac ttccctgagc 2760
agtgagaacc catatgccac catccggac ctgcccagct tgccaggggg ccccccggag 2820
agcagctaca tggagatgaa aggcctccc tcagtagatctc ccccccaggca gcctcctcag 2880
ttctgggaca gccagaggcg gcggcaaccc cagccacaga gagacagtgg cacctacgag 2940
cagcccagcc ccctgatcca tgaccgagac tctgtggct cccagccccc tctgcctccg 3000
ggcctacccc cggccacta tgactcaccc aagaacagcc acatccctgg acattatgac 3060
ttgcctccag tacggcatcc cccatcacct ccacttcgac gccaggaccg ttga 3114

<210> 10
<211> 1037
<212> PRT
<213> Homo sapiens

<400> 10
Met Ser Pro Pro Leu Cys Pro Leu Leu Leu Ala Val Gly Leu Arg
1 5 10 15

Leu Ala Gly Thr Leu Asn Pro Ser Asp Pro Asn Thr Cys Ser Phe Trp
20 25 30

Glu Ser Phe Thr Thr Thr Lys Glu Ser His Ser Arg Pro Phe Ser
35 40 45

Leu Leu Pro Ser Glu Pro Cys Glu Arg Pro Trp Glu Gly Pro His Thr
50 55 60

Cys Pro Gln Pro Thr Val Val Tyr Arg Thr Val Tyr Arg Gln Val Val
65 70 75 80

Lys Thr Asp His Arg Gln Arg Leu Gln Cys Cys His Gly Phe Tyr Glu
85 90 95

Ser Arg Glu Phe Cys Val Pro Leu Cys Ala Gln Glu Cys Val His Gly
100 105 110

Arg Cys Val Ala Pro Asn Gln Cys Gln Cys Val Pro Gly Trp Arg Gly
115 120 125

Asp Asp Cys Ser Ser Glu Cys Ala Pro Gly Met Trp Gly Pro Gln Cys
130 135 140

Asp Lys Pro Cys Ser Cys Gly Asn Asn Ser Ser Cys Asp Pro Lys Ser
145 150 155 160

Gly Val Cys Ser Cys Pro Ser Gly Leu Gln Pro Pro Asn Cys Leu Gln
165 170 175

Pro Cys Thr Pro Gly Tyr Tyr Gly Pro Ala Cys Gln Phe Arg Cys Gln
180 185 190

Cys His Gly Ala Pro Cys Asp Pro Gln Thr Gly Ala Cys Phe Cys Pro
195 200 205

Ala Glu Arg Thr Gly Pro Ser Cys Asp Val Ser Cys Ser Gln Gly Thr
210 215 220

Ser Gly Phe Phe Cys Pro Ser Thr His Pro Cys Gln Asn Gly Gly Val
225 230 235 240

Phe Gln Thr Pro Gln Gly Ser Cys Ser Cys Pro Pro Gly Trp Met Gly
245 250 255

Thr Ile Cys Ser Leu Pro Cys Pro Glu Gly Phe His Gly Pro Asn Cys
260 265 270

Ser Gln Glu Cys Arg Cys His Asn Gly Gly Leu Cys Asp Arg Phe Thr
275 280 285

Gly Gln Cys Arg Cys Ala Pro Gly Tyr Thr Gly Asp Arg Cys Arg Glu
290 295 300

Glu Cys Pro Val Gly Arg Phe Gly Gln Asp Cys Ala Glu Thr Cys Asp
305 310 315 320

Cys Ala Pro Asp Ala Arg Cys Phe Pro Ala Asn Gly Ala Cys Leu Cys
325 330 335

Glu His Gly Phe Thr Gly Asp Arg Cys Thr Asp Arg Leu Cys Pro Asp
340 345 350

Gly Phe Tyr Gly Leu Ser Cys Gln Ala Pro Cys Thr Cys Asp Arg Glu
355 360 365

His Ser Leu Ser Cys His Pro Met Asn Gly Glu Cys Ser Cys Leu Pro
370 375 380

Gly Trp Ala Gly Leu His Cys Asn Glu Ser Cys Pro Gln Asp Thr His
385 390 395 400

Gly Pro Gly Cys Gln Glu Tyr Cys Leu Cys Leu His Gly Gly Val Cys
405 410 415

Gln Ala Thr Ser Gly Leu Cys Gln Cys Ala Pro Gly Tyr Thr Gly Pro
 420 425 430

His Cys Ala Ser Leu Cys Pro Pro Asp Thr Tyr Gly Val Asn Cys Ser
 435 440 445

Ala Arg Cys Ser Cys Glu Asn Ala Ile Ala Cys Ser Pro Ile Asp Gly
 450 455 460

Glu Cys Val Cys Lys Glu Gly Trp Gln Arg Gly Asn Cys Ser Val Pro
 465 470 475 480

Cys Pro Pro Gly Thr Trp Gly Phe Ser Cys Asn Ala Ser Cys Gln Cys
 485 490 495

Ala His Glu Ala Val Cys Ser Pro Gln Thr Gly Ala Cys Thr Cys Thr
 500 505 510

Pro Gly Trp His Gly Ala His Cys Gln Leu Pro Cys Pro Lys Gly Gln
 515 520 525

Phe Gly Glu Gly Cys Ala Ser Arg Cys Asp Cys Asp His Ser Asp Gly
 530 535 540

Cys Asp Pro Val His Gly Arg Cys Gln Cys Gln Ala Gly Trp Met Gly
 545 550 555 560

Ala Arg Cys His Leu Ser Cys Pro Glu Gly Leu Trp Gly Val Asn Cys
 565 570 575

Ser Asn Thr Cys Thr Cys Lys Asn Gly Gly Thr Cys Leu Pro Glu Asn
 580 585 590

Gly Asn Cys Val Cys Ala Pro Gly Phe Arg Gly Pro Ser Cys Gln Arg
 595 600 605

Ser Cys Gln Pro Gly Arg Tyr Gly Lys Arg Cys Val Pro Cys Lys Cys
 610 615 620

Ala Asn His Ser Phe Cys His Pro Ser Asn Gly Thr Cys Tyr Cys Leu
 625 630 635 640

Ala Gly Trp Thr Gly Pro Asp Cys Ser Gln Pro Cys Pro Pro Gly His
 645 650 655

Trp Gly Glu Asn Cys Ala Gln Thr Cys Gln Cys His His Gly Gly Thr
 660 665 670

Cys His Pro Gln Asp Gly Ser Cys Ile Cys Pro Leu Gly Trp Thr Gly
675 680 685

His His Cys Leu Glu Gly Cys Pro Leu Gly Thr Phe Gly Ala Asn Cys
690 695 700

Ser Gln Pro Cys Gln Cys Gly Pro Gly Glu Lys Cys His Pro Glu Thr
705 710 715 720

Gly Ala Cys Val Cys Pro Pro Gly His Ser Gly Ala Pro Cys Arg Ile
725 730 735

Gly Ile Gln Glu Pro Phe Thr Val Met Pro Thr Thr Pro Val Ala Tyr
740 745 750

Asn Ser Leu Gly Ala Val Ile Gly Ile Ala Val Leu Gly Ser Leu Val
755 760 765

Val Ala Leu Val Ala Leu Phe Ile Gly Tyr Arg His Trp Gln Lys Gly
770 775 780

Lys Glu His His Leu Ala Val Ala Tyr Ser Ser Gly Arg Leu Asp
785 790 795 800

Gly Ser Glu Tyr Val Met Pro Asp Val Pro Pro Ser Tyr Ser His Tyr
805 810 815

Tyr Ser Asn Pro Ser Tyr His Thr Leu Ser Gln Cys Ser Pro Asn Pro
820 825 830

Pro Pro Pro Asn Lys Val Pro Gly Pro Leu Phe Ala Ser Leu Gln Asn
835 840 845

Pro Glu Arg Pro Gly Gly Ala Gln Gly His Asp Asn His Thr Thr Leu
850 855 860

Pro Ala Asp Trp Lys His Arg Arg Glu Pro Pro Pro Gly Pro Leu Asp
865 870 875 880

Arg Gly Ser Ser His Leu Asp Arg Ser Tyr Ser Tyr Ser Tyr Ser Asn
885 890 895

Gly Pro Gly Pro Phe Tyr Asp Lys Gly Leu Ile Ser Glu Glu Leu
900 905 910

Gly Ala Ser Val Thr Ser Leu Ser Ser Glu Asn Pro Tyr Ala Thr Ile
915 920 925

Arg Asp Leu Pro Ser Leu Pro Gly Gly Pro Arg Glu Ser Ser Tyr Met
930 935 940

Glu Met Lys Gly Pro Pro Ser Gly Ser Pro Pro Arg Gln Pro Pro Gln
945 950 955 960

Phe Trp Asp Ser Gln Arg Arg Arg Gln Pro Gln Pro Gln Arg Asp Ser
965 970 975

Gly Thr Tyr Glu Gln Pro Ser Pro Leu Ile His Asp Arg Asp Ser Val
980 985 990

Gly Ser Gln Pro Pro Leu Pro Pro Gly Leu Pro Pro Gly His Tyr Asp
995 1000 1005

Ser Pro Lys Asn Ser His Ile Pro Gly His Tyr Asp Leu Pro Pro Val
1010 1015 1020

Arg His Pro Pro Ser Pro Pro Leu Arg Arg Gln Asp Arg
1025 1030 1035

<210> 11

<211> 1833

<212> DNA

<213> Homo sapiens

<400> 11

agcgagtcgg tctgtcaggg cgcctcctct ccggccgtct gattttctac ctttcggcgc 60
cctgcttcc tcatagttgg catccccggc cacggagacc accgtccctca tgtcccaagac 120
tgaggccgac ctggccctgc ggccccggcc tcctcttggc accgcggggc agccccgcct 180
cggggccccc cctcgccgag cgccgcgtt ctccggaaag gctgagcccc ggccgcgc 240
ttcgagacct agccggcgca gctcagtcga tctggactg ctgagctcct ggtctcaacc 300
agcctcactc cttccggAAC ccccgatcc tccagactcc gctggcccca cgaggagccc 360
accttcaagc tctaaagaac ccccccgggg cacatggatg ggggcagctc ccgtgaaggc 420
tgtggactct gcatgtcctg agcttacggg atttcaggg ggcccggggt ccagggagcc 480
gctaagggtc cctgaagctg tggccctaga gcggcgccgg gagcagggaa aaaaaggagga 540
catggagacc caggctgtgg caacgtcccc cgatggccga tacctcaagt ttgacatcga 600
gattggacgt ggctccttca agacgggtta tcgagggtca gacaccgaca ccacagtgg 660
ggtgtggctgg tgtgagctgc agactcgaa actgtctaga gctgagccgc agcgcttctc 720
agaggaggtg gagatgtca aggggctgca gcaccccaac atcgccgtc tctatgattc 780
gtgaaagtgc gtgctgaggg gcccagggtt catcgtctg gtcaccgaac tcatgacctc 840
gggcacgctc aagacgtacc tgaggcggtt ccgggagatg aagccgcggg tccttcagcg 900
ctggagccgc caaatcctgc ggggacttca ttccctacac tcccggttcc ctcccatcct 960
gcacccggat ctcaagtgcg acaatgtctt tatcacggga cctactggct ctgtcaaaat 1020
cggggacctg ggcctggcca cgctcaagcg cgccctcctt gccaagagtg tcatcgggac 1080
cccggaattc atggcccccg agatgtacga ggaaaagtac gatgaggccg tggacgtgta 1140

cgcgttcggc atgtgcattgc tggagatggc cacctctgag taccgtact ccgagtgcca 1200
gaatgcccgcaaaatctacc gcaaggctcac ttccggcaga aagccgaaaca gcttccacaa 1260
ggtgaagata cccgaggtga aggagatcat tgaaggctgc atccgcacgg ataagaacga 1320
gaggttcacc atccaggacc tcctggccca cgcccttcttc cgcgaggagc gcggtgtgca 1380
cgtggaacta gcggaggagg acgacggcga gaagccgggc ctcaagctct ggctgcgcatt 1440
ggaggacgcgcggcgggg ggcgcacgg ggacaaccag gccatcgagt tcctgttcca 1500
gctggccgg gacgcggccg aggaggtggc acaggagatg gtggctctgg gcttggtctg 1560
tgaagccgat taccagccag tggccgtgc agtacgtgaa cgggttgctg ccatccagcg 1620
aaagcgtgag aagctgcgtaa aagcaaggaa attggaggca ctccaccag accaggacc 1680
tccaccagca actgtgcccatttgc tggacccgg tccaccaaca gatgtctatc caccatcata 1740
gacctgagga gcaagaggca agaccagaac acagcacattt ctttattaca gacacgcca 1800
gctactcatc taccacttcg gattgcgaga ctg 1833

<210> 12

<211> 557

<212> PRT

<213> Homo sapiens

<400> 12

Met Leu Ala Ser Pro Ala Thr Glu Thr Thr Val Leu Met Ser Gln Thr
1 5 10 15

Glu Ala Asp Leu Ala Leu Arg Pro Pro Pro Pro Leu Gly Thr Ala Gly
20 25 30

Gln Pro Arg Leu Gly Pro Pro Pro Arg Arg Ala Arg Arg Phe Ser Gly
35 40 45

Lys Ala Glu Pro Arg Pro Arg Ser Ser Arg Pro Ser Arg Arg Ser Ser
50 55 60

Val Asp Leu Gly Leu Leu Ser Ser Trp Ser Gln Pro Ala Ser Leu Leu
65 70 75 80

Pro Glu Pro Pro Asp Pro Pro Asp Ser Ala Gly Pro Thr Arg Ser Pro
85 90 95

Pro Ser Ser Ser Lys Glu Pro Pro Glu Gly Thr Trp Met Gly Ala Ala
100 105 110

Pro Val Lys Ala Val Asp Ser Ala Cys Pro Glu Leu Thr Gly Ser Ser
115 120 125

Gly Gly Pro Gly Ser Arg Glu Pro Leu Arg Val Pro Glu Ala Val Ala
130 135 140

Leu Glu Arg Arg Glu Gln Glu Glu Lys Glu Asp Met Glu Thr Gln

145 150 155 160
Ala Val Ala Thr Ser Pro Asp Gly Arg Tyr Leu Lys Phe Asp Ile Glu
165 170 175
Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Arg Gly Leu Asp Thr Asp
180 185 190
Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Thr Arg Lys Leu Ser
195 200 205
Arg Ala Glu Arg Gln Arg Phe Ser Glu Glu Val Glu Met Leu Lys Gly
210 215 220
Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Lys Ser Val
225 230 235 240
Leu Arg Gly Gln Val Cys Ile Val Leu Val Thr Glu Leu Met Thr Ser
245 250 255
Gly Thr Leu Lys Thr Tyr Leu Arg Arg Phe Arg Glu Met Lys Pro Arg
260 265 270
Val Leu Gln Arg Trp Ser Arg Gln Ile Leu Arg Gly Leu His Phe Leu
275 280 285
His Ser Arg Val Pro Pro Ile Leu His Arg Asp Leu Lys Cys Asp Asn
290 295 300
Val Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp Leu Gly
305 310 315 320
Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile Gly Thr
325 330 335
Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp Glu Ala
340 345 350
Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala Thr Ser
355 360 365
Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Tyr Arg Lys
370 375 380
Val Thr Ser Gly Arg Lys Pro Asn Ser Phe His Lys Val Lys Ile Pro
385 390 395 400
Glu Val Lys Glu Ile Ile Glu Gly Cys Ile Arg Thr Asp Lys Asn Glu

405	410	415
Arg Phe Thr Ile Gln Asp Leu Leu Ala His Ala Phe Phe Arg Glu Glu		
420	425	430
Arg Gly Val His Val Glu Leu Ala Glu Glu Asp Asp Gly Glu Lys Pro		
435	440	445
Gly Leu Lys Leu Trp Leu Arg Met Glu Asp Ala Arg Arg Gly Gly Arg		
450	455	460
Pro Arg Asp Asn Gln Ala Ile Glu Phe Leu Phe Gln Leu Gly Arg Asp		
465	470	475
Ala Ala Glu Glu Val Ala Gln Glu Met Val Ala Leu Gly Leu Val Cys		
485	490	495
Glu Ala Asp Tyr Gln Pro Val Ala Arg Ala Val Arg Glu Arg Val Ala		
500	505	510
Ala Ile Gln Arg Lys Arg Glu Lys Leu Arg Lys Ala Arg Glu Leu Glu		
515	520	525
Ala Leu Pro Pro Glu Pro Gly Pro Pro Pro Ala Thr Val Pro Met Asp		
530	535	540
Pro Gly Pro Pro Thr Asp Val Tyr Pro Pro His Glu Thr		
545	550	555

<210> 13

<211> 2646

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1408)

<223> Where n is a or c or t or g.

<400> 13

aaactcacta aaaataacaa aaggacagaa tgggtcccggt gggtccaagg caaagcatgg 60
ttcggttgct ccagatatgg tgcagtgcct cagctgctca ctgaagttcc ctctggcagg 120
aacgggtgctc tagatgggtt ttgtcaatct agataaaactt taatggttt cagtagattt 180
ctctatattt tgcagtagat tataaaatac ataatgtata tatacagtct atatatttgt 240
aaaaaaaaat taaagatatt tctaggtAAC accagtctgt ccttgaatta ccaaattttc 300
aaaagtctct aaagaaaaac ccagcaaatt tattttcaaa tacatctgtg tggagccaa 360
tccaaagtggg ctcacatggg tggatgtccac atttccatc tgctgtgcgt ggcatgttca 420

aatgctctgg gttgattatg cagggctgga tgctggcat gttcaa atgc tctgggttga 480
ttatgcaggg ctggattttg tgctcttgc cttggacag gagcttggga ttgtgggtct 540
ggagagaatc aaaatctgga ccacagcaca gttcatctt tgcttcatgg aattagaggc 600
aagactagag caagtgaagc agaaacaaag catcaattgc taggttcaaa gacaaccatg 660
tcctgtttct ccgtatgaca tctgacttgc catatacatg acgcagtttgc ttatctgtc 720
agagttacta catggttgtt ggaactaaac aagtaataaa taattgaagt tctgtcctct 780
cccatcactg tcagttattga tgtcttcctc aggtgcagta gagatgggag caaccaatga 840
cagcacccctc agccatttca tccttataagg cttctctgac cggcccgagc tggagagggt 900
cctcttcgcc atcatcctgc ccgcctacccct cctaaccctg ctgggcaaca gcatcatcat 960
cctggtatcc aggctggacc cgcacccctca cacccttgcg tacttcttgc tcacacaccc 1020
gtccttcctt gacccatgt tcaccaggtag ctccatccca cagctactct ataaacccatg 1080
cgggcccggac aagaccatca gctatgtggg ctgtgctctg cagctggtcc tggccttggg 1140
cctgggggggt gtggagtgcc tgcgtctggc tgcgtatggcc tatgaccgct ttgtggcggt 1200
ctgcaagccc ctgcactaca tggtcatcat gaaccccccag ctctgcccgg gcttgggtgc 1260
agtgacctgg ggctgtgggg tggcaactc cttggccatg ttcctgtga ccctgcgcctt 1320
accccgctgt gggcaccacg aggtggacca cttccatgtcgt gagatggccg ccctgatccg 1380
gatggcctgc gtcagcactg tggccatnga aggacccgtc tttgtcctgg cgggtgggtgc 1440
tgcctctgtcc cccttgggtgt ttatcatgt atcttacagc tacattgtga gggctgtgtt 1500
acaaattccgg tcagcatcag gaaggcagaa ggccctcggc acctgcggct cccatctcac 1560
tgtggtctcc cttttctatg gaaacatcat ctacatgtac atgcagccag gagccagttc 1620
ttcccaaggac cagggcaagt tcctcacgt ctcttacaac attgtcaccc ccctcctcaa 1680
tcctctcatc tacaccctca gaaacagaga ggtgaagggg gcactggaa ggttgcttct 1740
ggggaaagaga gagctaggaa aggagtaaag gcacatccac ctgacttcac ctccatccag 1800
ggccactggc agcatctgga acggctgaat tccagctgat attagccac gactcccaac 1860
ttgcctttt ctggactttt gtgaggctgt ttcaagtctg acattatgtg ttttgggtgt 1920
tgcctttaaa attgagacgg ggtctactc tgcacccat ggtggagtgc agtggtgcca 1980
ccatagctcc ttgcactatt gggcttaagc gatccctcccc cacctcagcc ttccaagtaa 2040
ctgggactac aggtgtgcat cactggcagt gggaaattgtg gctttctgt ctctatggc 2100
gacggggctt tgctgtgtt accaggctgg tcccaaaact cctggcctca tgcgtatcc 2160
ctgccatggc ctcctaaagt tctgggatca caagtgtgag tcactgtgac tggccaaat 2220
tatgtgattt atgtgtgaac tatataacac aaatcatccc caaaaccat catgatctgt 2280
aaagcagctg caaagaatga agtgagagaa acagttgtaa agatgagttt ccacctactt 2340
ataccagagt gctaagagga aataactt ctcaatcaga gctttgttt gtttgggtgtt 2400
gtttgttta aagtctaaaca cacctgacat gttcagtca gaatgacccc aaatgcata 2460
ctgttctcca cgtggtccaa gtgcctctt gtttagggcc atcaaatcat ggaatgcagc 2520
acagtttgat attttctata ttcccaattc ctacccaaac cttttcatga aatcgtagag 2580
tttgggggttac cctttatctg gtgttaagatt ctgcataaaac caagaagtga acctgtata 2640
tctatc 2646

<210> 14
<211> 322
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (203)

<223> Where Xaa is Ile or Met

<400> 14

Met Ser Ser Ser Gly Ala Val Glu Met Gly Ala Thr Asn Asp Ser Thr
1 5 10 15

Phe Ser His Phe Ile Leu Ile Gly Phe Ser Asp Arg Pro Glu Leu Glu
20 25 30

Arg Val Leu Phe Ala Ile Ile Leu Pro Ala Tyr Leu Leu Thr Leu Leu
35 40 45

Gly Asn Ser Ile Ile Ile Leu Val Ser Arg Leu Asp Pro His Leu His
50 55 60

Thr Pro Met Tyr Phe Phe Leu Thr His Leu Ser Phe Leu Asp Leu Ser
65 70 75 80

Phe Thr Ser Ser Ser Ile Pro Gln Leu Leu Tyr Asn Leu Ser Gly Pro
85 90 95

Asp Lys Thr Ile Ser Tyr Val Gly Cys Ala Leu Gln Leu Val Leu Phe
100 105 110

Leu Gly Leu Gly Gly Val Glu Cys Leu Leu Leu Ala Val Met Ala Tyr
115 120 125

Asp Arg Phe Val Ala Val Cys Lys Pro Leu His Tyr Met Val Ile Met
130 135 140

Asn Pro Gln Leu Cys Arg Gly Leu Val Ser Val Thr Trp Gly Cys Gly
145 150 155 160

Val Ala Asn Ser Leu Ala Met Ser Pro Val Thr Leu Arg Leu Pro Arg
165 170 175

Cys Gly His His Glu Val Asp His Phe Leu Arg Glu Met Pro Ala Leu
180 185 190

Ile Arg Met Ala Cys Val Ser Thr Val Ala Xaa Glu Gly Thr Val Phe
195 200 205

Val Leu Ala Val Gly Ala Ala Leu Ser Pro Leu Val Phe Ile Met Ile
210 215 220

Ser Tyr Ser Tyr Ile Val Arg Ala Val Leu Gln Ile Arg Ser Ala Ser
225 230 235 240

Gly Arg Gln Lys Ala Phe Gly Thr Cys Gly Ser His Leu Thr Val Val
245 250 255

Ser Leu Phe Tyr Gly Asn Ile Ile Tyr Met Tyr Met Gln Pro Gly Ala
260 265 270

Ser Ser Ser Gln Asp Gln Gly Lys Phe Leu Thr Leu Phe Tyr Asn Ile
275 280 285

Val Thr Pro Leu Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Arg Glu
290 295 300

Val Lys Gly Ala Leu Gly Arg Leu Leu Leu Gly Lys Arg Glu Leu Gly
305 310 315 320

Lys Glu

<210> 15

<211> 2381

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (2004)

<223> Where n is a or c or t or g.

<400> 15

ggaaaaattg acgggaggga agagggtgga gagcaggaca gagagggcgg tgcaagaagg 60
gaatatccct cctgagttcc ctggaagagc gtcagcctgg accctggtct tgggcttctc 120
tgctggaatc ctggcagcc ccgggtgctg cggcgagggt caaggccaca caaaggcaca 180
ggcaggcaga cgagccagtc acatggggca gtcgagctgc ctgcgtaat gctaggcgcg 240
ggacaatggc aactccggga caaagtgcag ggagactct gaagagataa gagggaaagg 300
cgaaggaagg gggcggggag ccagagcctc ggagctccag gaccgcgtt tggagaccg 360
tggctggaag ccgagctcgg cccgctgcgg aaggggcgcc ctcgcgcctc tacactctag 420
ccccggctgg gatgctgaga accgcggctt ccagggccgc aggcgagctc ccagccagtc 480
cccgccccc cccttcggtg ctggaggcgg ggctgcccag ctcacctggc cgtttgggt 540
gggaccgccc gcgaccgggg ggagctgcag aggcggccgtt acccagggaa gtggagctgg 600
gcttgccctg gggacttggc tggagctcac acccctccac gccccccaag gcctgcgcgg 660
gggcctccc ctatccct ccctccctt cctccctc ctcctctt ctttgcctc 720
ctccctccga acccaattgc tcaagcagct tcctccca acgccagcgc cagttccct 780
cccggtgggg cccggaaagg gcagctaact ctggacactg ggacggccgc ggcggcagct 840
tcaagaccat ggcccagctc ggagggggcg cgaaccggcc accccacggcc tctctgcgc 900
cgacctcgca gagcctgcgg tgcccccgc agccccccc ctcgagagcg gacactggta 960
gcctggcag gtactggggc aaagccgcag cccgcgcctc ccgggagcac cccttcccag 1020
gcacgctgat gcactctgca gcgccgtcag ggcggccgc gggagcgcgtg cgccaactgc 1080

tggggctgca gcgggcggct cctgcggggt ggctgtcgga ggagcgcgcc gaggagctgg 1140
gcgggcccagag tggggccgggc agcagcaggc tgcgtcgga accgcgggag cacgcgtgga 1200
ttctggcagc cgccgagggc cgctatgagg tgctgcggga gctgctggag gctgagccgg 1260
agctgctgct gaggggcgac ccgatcaccg gctactcggt tctgcactgg ctggccaagc 1320
acggggcgcac cgaggagctc attctggta acgacttcgc cctacgcggg gggctgaggc 1380
tcgacgtgag cgcccccaggc agcggcggcc tcacgcggc ccacctggcg gcccttcagg 1440
gccacgacat ggtcatcaag gtgctggtgg gcgcgcggg tgctgacgct acgcgcgcg 1500
accacagcgg ccaccgggccc tgccactacc tgccgcggcga cgccgcggcgg agggtgcggg 1560
agctgtcggg agccgaggaa tgggagatgg agagcggcag cgggtgcacc aacctaaca 1620
acaacagcag cggcaccact gcgtggaggg cccgcgcgc agtggggcgc gaacggctgt 1680
ggagacaagc aggagagtg cagcgtcgcc gaccaaggcg aaggacaccg cgggcagccg 1740
gttggcgcgg atgcatacgcc tttccgcgc tctgttcccc tcattccagg accgttgaca 1800
gggacagaga ctggagagct aggaggggct gtgacactgt ggcgatggct aggtcctggg 1860
ttgttcccggg ttccaccgaa ggagaggcgc cttggacgct gcttggcgc gcaaggaaca 1920
gaacacgtcg gggtccgact caggtacttg tctcaggtct cctgtaaacca ccggcctgg 1980
ggacccgggg actcgggcac cacntcacca agagagatg aaggaccaag ctggcctggc 2040
tccgagttcc aaagctacag gactaaggag ttgggagcag ggagcgtgg cctgttggg 2100
agagggcaag ttaagcttcc aggggcatt tctggcagg ccgacgcgc gggtttatta 2160
gaaacacattc gctagaagaa tgagttaaga ttgtaaacca ccaatgcaga gaaaacgcct 2220
aactctgccc gcctcgctcg gccattaaatg ggttgggg tgccggtaga gtcagcctct 2280
gacaacctcc tcctgagacg acccagcctt actggactt tttctcatgt atcacaggtt 2340
acttctttagt tatattaaag tggatatgt gttctttca c 2381

<210> 16
<211> 372
<212> PRT
<213> Homo sapiens

<400> 16

Met Ala Gln Leu Gly Gly Ala Ala Asn Arg Ala Pro Thr Ala Ser Leu
1 5 10 15

Ala Pro Thr Ser Gln Ser Leu Arg Cys Ala Pro Gln Pro Arg Pro Ser
20 25 30

Arg Ala Asp Thr Gly Ser Leu Gly Arg Tyr Trp Gly Lys Ala Ala Ala
35 40 45

Ala Ala Ser Arg Glu His Pro Phe Pro Gly Thr Leu Met His Ser Ala
50 55 60

Ala Gly Ser Gly Arg Arg Gly Ala Leu Arg Glu Leu Leu Gly Leu
65 70 75 80

Gln Arg Ala Ala Pro Ala Gly Trp Leu Ser Glu Glu Arg Ala Glu Glu
85 90 95

Leu Gly Gly Pro Ser Gly Pro Gly Ser Ser Arg Leu Cys Leu Glu Pro
 100 105 110
 Arg Glu His Ala Trp Ile Leu Ala Ala Ala Glu Gly Arg Tyr Glu Val
 115 120 125
 Leu Arg Glu Leu Leu Glu Ala Glu Pro Glu Leu Leu Arg Gly Asp
 130 135 140
 Pro Ile Thr Gly Tyr Ser Val Leu His Trp Leu Ala Lys His Gly Arg
 145 150 155 160
 His Glu Glu Leu Ile Leu Val His Asp Phe Ala Leu Arg Arg Gly Leu
 165 170 175
 Arg Leu Asp Val Ser Ala Pro Gly Ser Gly Gly Leu Thr Pro Leu His
 180 185 190
 Leu Ala Ala Leu Gln Gly His Asp Met Val Ile Lys Val Leu Val Gly
 195 200 205
 Ala Leu Gly Ala Asp Ala Thr Arg Arg Asp His Ser Gly His Arg Ala
 210 215 220
 Cys His Tyr Leu Arg Pro Asp Ala Pro Trp Arg Leu Arg Glu Leu Ser
 225 230 235 240
 Gly Ala Glu Glu Trp Glu Met Glu Ser Gly Ser Gly Cys Thr Asn Leu
 245 250 255
 Asn Asn Asn Ser Ser Gly Thr Thr Ala Trp Arg Ala Ala Ser Ala Val
 260 265 270
 Gly Arg Glu Arg Leu Trp Arg Gln Ala Gly Glu Trp Gln Arg Arg Gly
 275 280 285
 Pro Arg Arg Arg Thr Pro Arg Ala Ala Gly Trp Arg Lys Cys Ile Ala
 290 295 300
 Phe Ser Ala Ile Cys Ser Pro His Ser Arg Thr Val Asp Arg Asp Arg
 305 310 315 320
 Asp Trp Arg Ala Arg Arg Gly Cys Asp Thr Val Ala Met Ala Arg Ser
 325 330 335
 Trp Val Val Pro Gly Ser Thr Glu Gly Glu Ala Pro Trp Thr Leu Leu
 340 345 350

Gly Pro Ala Arg Asn Arg Thr Arg Arg Gly Pro Thr Gln Val Leu Val
355 360 365

Ser Gly Leu Leu
370

<210> 17
<211> 1209
<212> DNA
<213> Homo sapiens

<400> 17
agctaacgct ggacactggg acggccgcgg cggcagcttc aagaccatgg cccagctcg 60
agggggccgcg aaccgggcac ccacggcctc tctcgcgcgg acctcgcaga gcctgcggtg 120
cgcccccgcag cccccccct cgagagcgga cactggtagc ctgggcaggt actggggcaa 180
agccgcagcc gcccgcctcc gggagcaccc cttcccgagc acgctgatgc actctgcagc 240
gggctcaggg cgccggcggg gagcgcgtcg ggaactgctg gggctgcagc gggcggctcc 300
tgccgggtgg ctgtcggagg agcgcgcga ggagctggc gggccgagtg ggccgggcag 360
cagcaggctg tgccttggaaac cgcgggagca cgcgtggatt ctggcagccg ccgagggccg 420
ctatgaggtg ctgcgggagc tgctggaggc tgagccggag ctgctgctga gggcgaccc 480
gatcaccggc tactcggttc tgcaactggct ggccaagcac gggcgccacg aggagctcat 540
tctggtacac gacttcgccc tacgcccggg gctgaggctc gacgtgagcg ccccaggcag 600
cggcggcctc acgcgcctcc acctggcggc cttcaggc cacgacatgg tcatcaaggt 660
gctgggtggc gcccgggtg ctgacgctac gcgcgcgcac cacagcggcc accgggcctg 720
ccactacctg cggccgcacg cgccttggag gttgcggag ctgtcggag ccgaggaatg 780
ggagatggag agcggcagcg ggtgcaccaa cctgaacaac aacagcagcg gcaccactgc 840
gtggaggggc gcgcgcgcac tggcgcgcac ggctgtggag acaagcagga gagtggcagc 900
gtcgcggacc aaggcgaagg acaccgcggg cagccgggtg gcgcaaatgc atagccttt 960
ccgccccatctg ttccccat tccaggaccg ttgacaggga cagagactgg agagcttagga 1020
ggggctgtga cactgtggcg atggcttaggt cctgggttc cccgggttc accgaaggag 1080
aggcgccttg gacgctgctt gggcctgcaaa ggaacagaac acgtcggggt ccgactcagg 1140
tacttgtctc aggtctcctg taaccaccgg cctggaggac ccggggactc gggcaccact 1200
tcaccaaga 1209

<210> 18
<211> 315
<212> PRT
<213> Homo sapiens

<400> 18
Met Ala Gln Leu Gly Gly Ala Ala Asn Arg Ala Pro Thr Ala Ser Leu
1 5 10 15

Ala Pro Thr Ser Gln Ser Leu Arg Cys Ala Pro Gln Pro Arg Pro Ser
20 25 30

Arg Ala Asp Thr Gly Ser Leu Gly Arg Tyr Trp Gly Lys Ala Ala Ala
 35 40 45

Ala Ala Ser Arg Glu His Pro Phe Pro Gly Thr Leu Met His Ser Ala
 50 55 60

Ala Gly Ser Gly Arg Arg Gly Ala Leu Arg Glu Leu Leu Gly Leu
 65 70 75 80

Gln Arg Ala Ala Pro Ala Gly Trp Leu Ser Glu Glu Arg Ala Glu Glu
 85 90 95

Leu Gly Gly Pro Ser Gly Pro Gly Ser Ser Arg Leu Cys Leu Glu Pro
 100 105 110

Arg Glu His Ala Trp Ile Leu Ala Ala Ala Glu Gly Arg Tyr Glu Val
 115 120 125

Leu Arg Glu Leu Leu Glu Ala Glu Pro Glu Leu Leu Leu Arg Gly Asp
 130 135 140

Pro Ile Thr Gly Tyr Ser Val Leu His Trp Leu Ala Lys His Gly Arg
 145 150 155 160

His Glu Glu Leu Ile Leu Val His Asp Phe Ala Leu Arg Arg Gly Leu
 165 170 175

Arg Leu Asp Val Ser Ala Pro Gly Ser Gly Gly Leu Thr Pro Leu His
 180 185 190

Leu Ala Ala Leu Gln Gly His Asp Met Val Ile Lys Val Leu Val Gly
 195 200 205

Ala Leu Gly Ala Asp Ala Thr Arg Arg Asp His Ser Gly His Arg Ala
 210 215 220

Cys His Tyr Leu Arg Pro Asp Ala Pro Trp Arg Leu Arg Glu Leu Ser
 225 230 235 240

Gly Ala Glu Glu Trp Glu Met Glu Ser Gly Ser Gly Cys Thr Asn Leu
 245 250 255

Asn Asn Asn Ser Ser Gly Thr Thr Ala Trp Arg Ala Ala Ser Ala Val
 260 265 270

Gly Ala Thr Ala Val Glu Thr Ser Arg Arg Val Ala Ala Ser Arg Thr
 275 280 285

Lys Ala Lys Asp Thr Ala Gly Ser Arg Val Ala Gln Met His Ser Leu
290 295 300

Phe Arg His Leu Phe Pro Ser Phe Gln Asp Arg
305 310 315

<210> 19
<211> 6272
<212> DNA
<213> Homo sapiens

<400> 19
aggacgatgc ccaagggtgg gtgcctaaa gcaccacagc aggaagagct tcccctcagc 60
agcgacatgg tggagaagca gactggaaa aagaaagata aagtttctt aaccaagacc 120
ccaaaactgg agcggtggcga tggcggaag gaggtgaggg agcgagccag caagcggaag 180
ctgccttca ccgcgggcgc caatggggag cagaaggact cggacacagg taccagcccg 240
acagccttac ctctgtgtga ccccttcaca tacactgcgg aagaaggccaa agctgaaagg 300
cagaaggcagg gcccgtggcg gaagaggatt aagaaggagc ctgtcaccgg gaaggccgg 360
ctgtctggaa tccgagccgg ctacccctc tccgagcgcc agcagggtggc ctttctcatg 420
cagatgacgg ccgaggagtc tgccaacagc ccagtggaca caacacccaa gcacccctcc 480
cagtctacag tgggtcgaaa gggAACGCC aactctgcct caaaaacccaa agataaagtg 540
aacaagagaa acgacgtgg agagaccgcg ctgcaccggc cggccatccg cggggacgc 600
cggcgcacatca aagagctcat cagcgagggg gcagacgtca acgtcaagga cttcgcaggc 660
tggacggcgc tgcacgaggc ctgttaaccgg ggctactacg acgtcgcgaa gcagctgctg 720
gctgcagggtg cggagggtgaa caccaagggc cttagatgacg acacgcctt gcacgacgct 780
gccaacaacg ggcaccagggt ggtgaagctg ctgtcgcgtt acggaggaa cccgcagcag 840
agcaacacgaa aaggcgagac gcccgtgaaa gtggccact ccccccacgat ggtgaacctc 900
ctgttagca aaggcactt cacttccagc gaggagagca gctcagaaga ggaagacgca 960
ccatccttcg caccttccag ttcaagtgcac ggcaacaaca cggactccga gttcgaaaaa 1020
ggcctaagc acaaggccaa gaacccagag ccacagaagg ccacggcccc cgtcaaggac 1080
gagtagatgtt ttgatgagga cgacgagcag gacagggttc ctccgggtgaa cgacaagcac 1140
ctattgaaaa aggactacag aaaagaaaacg aaatccaata gtttatctc tatacccaa 1200
atggaggtt aaagttcac taaaataac acgattgcac caaagaaaacg gtcccatcgt 1260
atcctgtcag acacgtcggc cgaggaggac gcgagtgta ccgtggggac aggagagaag 1320
ctgagactct cggcacatac gatattgcct ggttagtaaga cacgagagcc ttctaatgcc 1380
aaggcagcaga aggaaaaaaa taaagtgaaa aagaagcgaa agaaaagaaaac aaaaggcaga 1440
gagggtcgct tcggaaagcg gagcgacaag ttctgctcct cggagtcggc gagcgagtcc 1500
tcagagagtg gggaggatga cagggactct ctggggagct ctggctgcct caaggggtcc 1560
ccgctgggtgc tgaaggaccc ctccctgttc agctccctct ctgcctcctc cacctcgct 1620
cacgggagct ctggcccccga gaagcagaac gaccagcaca ccaagcactg gaaaaccatt 1680
tcttccccgg cttggtcaga ggtcaagtctt ttatcagact ccacaaggac gagactgaca 1740
agcgagtctg actactccctc tgagggctcc agtgtggaaat cgctgaagcc agtgaggaag 1800
aggcaggagc acaggaagcg agcctccctg tcggagaaga agagccctt cctgtccagc 1860
gcggaggcgc ctgtccccaa actggacaag gagggaaaag ttgtcaaaaa acataaaaaca 1920
aaacacaaac acaaaaaacaa ggagaagatc agccaagagc tgaagttgaa aagttttact 1980
tacgaatatg aggactccaa gcagaagtca gataaggcta tactgttaga gaatgatctt 2040
tccactgaaa acaagctaaa agtgttaaag cagcatcgcc accactttaa aaaaagaagag 2100

aaacttagca aaatgaaatt agaagaaaaa gaatggctct ttaaagatga aaaatcactg 2160
aagagaatca aagacaaact gagactgtac aaagaggaga gagacaaaat ttcaaaagag 2220
aaggagaaga tttttaaga agataaaagaa aaactcaaaa aagaaaaggt ttataggaa 2280
gatagcctt ctgaccggga ttcatccctt gattcaag gggcaagct catcttggag 2340
acggtaagg aggacagcaa ggagaggagg cgggacagcc gggccggga gaagcaccca 2400
gcacgagaga aggagaagcc cgataagagg aagagataca aagagaaaga caaggacaaa 2460
agtgagaaat caatcttggaa aaaatgtcag aagacaaag agaaaaaaaaga aaaacataaa 2520
gacacacatg gcaaagacaa agaaaggaaa gcgtctgtct ttgaaaagca caaggagaag 2580
aaggataaag agtccacaga aaagtacaag gacagaccc cagtgactc cacgcaagat 2640
aagaaaaata aacaggagaa ggctgaaaag aagcacgctg ccgaagacaa ggctaaaagc 2700
aaacacaaag agaagtcgga caaagaacat tccaaggaga ggaagtccctc gagaagtgcc 2760
gacgcggaat acagagaaag cgaggtctcc tctgacagct tcacggaccg agaggacgac 2820
aagagcgcct gcctccctga gaagctgaaa gagaagaggc acagacactc ctcatcttca 2880
tccaagaaga gccacgaccg agaggagaag aaagaggatt acaaggaggg caggaaggc 2940
cagtacgaaa aggaccttggaa ggcggatgct tacggagttt cttacaacat gaaagctatt 3000
gaattgtttg aaaagaaaga taaaaatgat gaacctctaa aagagaagaa gaagagagag 3060
aaacacaggg agaaatggag agacgagaag gagaggcacc gggacaggca tgccgatagg 3120
ccgaagccat ccaaagaccc aggcaagaaa gacgccaggc ccagggagaa gctcctgggg 3180
gacggcgacc tcatgtatgac cagcttcgag aggatgctgt cccagaagga cctggagatc 3240
gaggagcgcc acaagcggca caaggagagg atgaagcaaa tggagaagct gaggcaccgg 3300
tccggagacc ccaagctcaa ggagaaggcg aagccggcag acgacggcg gaagaagggt 3360
ctggacattc ctgctaagaa accgccccggg ctggaccctc catttaaaga caaaaagctc 3420
aaagagtcta ctcctattcc acctgcccgc gaaaataagc tacacccagc atcaggtgca 3480
gactccaaag actggctggc aggcctcac atgaaagagg tcctgcctgc gtccccccagg 3540
cctgaccaga gccggcccac tggcgtgccc acccctacgt cggctctatc ctgccccagc 3600
tacgaggagg tcatgtatgac gcccaggacc cctgcctgca gcccggatga ctacgcccggc 3660
ctcggtttcg actgcgcga ctcgcagcac tccacgcccc tgcccaccgc tcccaccagc 3720
gcctgctccc ctccttttt cgacagggtt tccgtggctt caagtgggt ttcggaaaac 3780
gccagccagg ctccgtccag gcctctctcc acaaaccctt accgctcggt ctctgtcgac 3840
attgacaagc tcttcaggca gcagagcggtt cctgctgcct ccagctacga ctctccatg 3900
ccaccctcga tggaaagacag ggcggccctg ccccccgttc cccggagaa gtttgcctgc 3960
ttgtcgccag ggtactactc cccagactat gcctcccggt cggccaaagt cgacgctttg 4020
caactgcccac cggctgcccgt tgcactgtc accccgtctc cagagggcgt ctctcaagt 4080
ttacaagcaa aacccccc ttcctccct tccctggaca cctccggagga ccagcaggcg 4140
acggccgcca tcatcccccc ggagcccagc tacctggagc cgctggacga gggcccttc 4200
agcgcgtca tcaccgagga gcccgttggag tggcccccacc cctccggagca ggcgttgcc 4260
tctagcctga tcgggggcac ctctgaaaac cctgtgagct ggcctgtggg ctccggaccc 4320
ctgctgaagt ctccacagag attccccgag tcccaaagc gtttctgccc cgccggacccc 4380
ctccactctg ccccccagg gccttcagc gcctcgagg cggccgtaccc cgcccccctccc 4440
gcctctctg ccccgtagc tctgccccgtc gctgagctgg aggacgtcaa ggacgtcccc 4500
gccgcctatct ccacctcaga ggcggctccc tacggccctc cctccgggtt ggagtccctc 4560
ttcagcaact gcaagtcaact tccggaaagcc cgcgtggacg tggcccccga ggctctgggg 4620
ccccctggaaa atagttccct ggacggcagc cgccggctgt ctccacctcg ccaggtggag 4680
ccggtgccct gggcggacgc ctgcggccgc cccgaggacg acctggaccc gggcccttc 4740
tccctggccgg agctccccct gcagactaaa gatggccgcag atggtaagc ggaacccgtg 4800
gaagaaagtc ttgctccctc agaagagatg cttccagggg ccccccggga gctcgagcc 4860
gagccctcag gggagccaaa gctggacgtg gctctagaag ctgcgggtggaa ggcggagacg 4920
gtggccggaaag agagggcccg tggggatccg gactccagcg tggagccccgc gcccgttccc 4980

ccagaacagc tggggagcgg agaccctcc ctctgtgccc ctgacggccc cgccccgaac 5040
 actgtggcac aagctcaggc cgcagacggt gccggccccc aggacgacac tgaggcctcc 5100
 cgtgccgcg ccccagccga aggccctcct ggccagccgg aagccgcaga accaaaaccc 5160
 acggccgaag ccccgaaggc ccccccagag atccctcagc gcatgaccag gaaccggcgg 5220
 cagatgctcg cgaaccagag caagcaggc cccggccccc ccgagaagga gtgcggcccc 5280
 acccctgccc cggtcaccag ggccaaggcc cgcggctccg aggacgacga cgcccaggcc 5340
 cagcatccgc gcaaacgccc ctccatcagc tccaccagc agctgcagct gaacacgtcc 5400
 acgcagcaga cgcgggaggt gatccagc acgctggccg ccatcgtgga cccatcaag 5460
 ctggatgcca tcgagcccta ccacagcgac aggccaacc cctacttcga atacctgcag 5520
 atcaggaaga agatcgagga gaagcgcaag atcctgtgct gtatcagcc gcaggcggcc 5580
 cagtgtacg ccgagtaagt cacctacacg ggctcctacc tcctggacgg caagccgctc 5640
 agcaagctcc acatccccgt gatcgacccc cctccctccc tggcggagcc cctgaaggag 5700
 ctgttcaggc agcaggagc cgtccgggaa aagctgcgtc tacagcacag catcgagcgg 5760
 gagaagctga tcgtatcctg tgagcaggag attctgcggg ttcaactgccc ggcggccagg 5820
 accatcgcca accaggcagt gccattcagc gcctgcacga tgctgctgga ctccgaggc 5880
 tacaacatgc ccctggagag ccaggggtgac gagaacaagt cagtgcgcga ccgttcaac 5940
 gcccggcagt tcatctcctg gctccaggac gtggatgaca agtatgaccg catgaaggc 6000
 tgcctcctca tgcggcagca gcacgagcc gcgccctga acgccgtgca gaggatggag 6060
 tggcagctga aggtgcagga actggacccc gccggcaca agtccctgtg cgtgaacgag 6120
 gtgccctctt tctacgtgcc catggtcgac gtcaacgacg actttgtatt gttgccggca 6180
 tgacaccgcg ggacggccgc aggacgcagg cgagggccgc acggctgccc aggactgctg 6240
 ctgagccccca gggcgggagg agggagcggcc ct 6272

<210> 20

<211> 2058

<212> PRT

<213> Homo sapiens

<400> 20

Met	Pro	Lys	Gly	Gly	Cys	Pro	Lys	Ala	Pro	Gln	Gln	Glu	Glu	Leu	Pro
1															

Leu	Ser	Ser	Asp	Met	Val	Glu	Lys	Gln	Thr	Gly	Lys	Lys	Lys	Asp	Lys
				20					25						30

Val	Ser	Leu	Thr	Lys	Thr	Pro	Lys	Leu	Glu	Arg	Gly	Asp	Gly	Gly	Lys

Glu	Val	Arg	Glu	Arg	Ala	Ser	Lys	Arg	Lys	Leu	Pro	Phe	Thr	Ala	Gly

Ala	Asn	Gly	Glu	Gln	Lys	Asp	Ser	Asp	Thr	Gly	Thr	Ser	Pro	Thr	Ala

Leu	Pro	Leu	Cys	Asp	Pro	Phe	Thr	Tyr	Thr	Ala	Glu	Glu	Ala	Lys	Ala

Glu Arg Gln Lys Gln Gly Pro Glu Arg Lys Arg Ile Lys Lys Glu Pro
100 105 110

Val Thr Arg Lys Ala Gly Leu Ser Gly Ile Arg Ala Gly Tyr Pro Leu
115 120 125

Ser Glu Arg Gln Gln Val Ala Leu Leu Met Gln Met Thr Ala Glu Glu
130 135 140

Ser Ala Asn Ser Pro Val Asp Thr Thr Pro Lys His Pro Ser Gln Ser
145 150 155 160

Thr Val Cys Gln Lys Gly Thr Pro Asn Ser Ala Ser Lys Thr Lys Asp
165 170 175

Lys Val Asn Lys Arg Asn Glu Arg Gly Glu Thr Arg Leu His Arg Ala
180 185 190

Ala Ile Arg Gly Asp Ala Arg Arg Ile Lys Glu Leu Ile Ser Glu Gly
195 200 205

Ala Asp Val Asn Val Lys Asp Phe Ala Gly Trp Thr Ala Leu His Glu
210 215 220

Ala Cys Asn Arg Gly Tyr Tyr Asp Val Ala Lys Gln Leu Leu Ala Ala
225 230 235 240

Gly Ala Glu Val Asn Thr Lys Gly Leu Asp Asp Asp Thr Pro Leu His
245 250 255

Asp Ala Ala Asn Asn Gly His Gln Val Val Lys Leu Leu Leu Arg Tyr
260 265 270

Gly Gly Asn Pro Gln Gln Ser Asn Arg Lys Gly Glu Thr Pro Leu Lys
275 280 285

Val Ala Asn Ser Pro Thr Met Val Asn Leu Leu Leu Gly Lys Gly Thr
290 295 300

Tyr Thr Ser Ser Glu Glu Ser Ser Glu Glu Glu Asp Ala Pro Ser
305 310 315 320

Phe Ala Pro Ser Ser Ser Val Asp Gly Asn Asn Thr Asp Ser Glu Phe
325 330 335

Glu Lys Gly Leu Lys His Lys Ala Lys Asn Pro Glu Pro Gln Lys Ala
340 345 350

Thr Ala Pro Val Lys Asp Glu Tyr Glu Phe Asp Glu Asp Asp Glu Gln
355 360 365

Asp Arg Val Pro Pro Val Asp Asp Lys His Leu Leu Lys Lys Asp Tyr
370 375 380

Arg Lys Glu Thr Lys Ser Asn Ser Phe Ile Ser Ile Pro Lys Met Glu
385 390 395 400

Val Lys Ser Tyr Thr Lys Asn Asn Thr Ile Ala Pro Lys Lys Ala Ser
405 410 415

His Arg Ile Leu Ser Asp Thr Ser Asp Glu Glu Asp Ala Ser Val Thr
420 425 430

Val Gly Thr Gly Glu Lys Leu Arg Leu Ser Ala His Thr Ile Leu Pro
435 440 445

Gly Ser Lys Thr Arg Glu Pro Ser Asn Ala Lys Gln Gln Lys Glu Lys
450 455 460

Asn Lys Val Lys Lys Arg Lys Glu Thr Lys Gly Arg Glu Val
465 470 475 480

Arg Phe Gly Lys Arg Ser Asp Lys Phe Cys Ser Ser Glu Ser Glu Ser
485 490 495

Glu Ser Ser Glu Ser Gly Glu Asp Asp Arg Asp Ser Leu Gly Ser Ser
500 505 510

Gly Cys Leu Lys Gly Ser Pro Leu Val Leu Lys Asp Pro Ser Leu Phe
515 520 525

Ser Ser Leu Ser Ala Ser Ser Thr Ser Ser His Gly Ser Ser Ala Ala
530 535 540

Gln Lys Gln Asn Asp Gln His Thr Lys His Trp Lys Thr Ile Ser Ser
545 550 555 560

Pro Ala Trp Ser Glu Val Ser Ser Leu Ser Asp Ser Thr Arg Thr Arg
565 570 575

Leu Thr Ser Glu Ser Asp Tyr Ser Ser Glu Gly Ser Ser Val Glu Ser
580 585 590

Leu Lys Pro Val Arg Lys Arg Gln Glu His Arg Lys Arg Ala Ser Leu
595 600 605

Ser Glu Lys Lys Ser Pro Phe Leu Ser Ser Ala Glu Gly Ala Val Pro
610 615 620

Lys Leu Asp Lys Glu Gly Lys Val Val Lys Lys His Lys Thr Lys His
625 630 635 640

Lys His Lys Asn Lys Glu Lys Ile Ser Gln Glu Leu Lys Leu Lys Ser
645 650 655

Phe Thr Tyr Glu Tyr Glu Asp Ser Lys Gln Lys Ser Asp Lys Ala Ile
660 665 670

Leu Leu Glu Asn Asp Leu Ser Thr Glu Asn Lys Leu Lys Val Leu Lys
675 680 685

His Asp Arg Asp His Phe Lys Lys Glu Lys Leu Ser Lys Met Lys
690 695 700

Leu Glu Glu Lys Glu Trp Leu Phe Lys Asp Glu Lys Ser Leu Lys Arg
705 710 715 720

Ile Lys Asp Lys Leu Arg Leu Tyr Lys Glu Glu Arg Asp Lys Ile Ser
725 730 735

Lys Glu Lys Glu Lys Ile Phe Lys Glu Asp Lys Glu Lys Leu Lys Lys
740 745 750

Glu Lys Val Tyr Arg Glu Asp Ser Leu Ser Asp Arg Asp Ser Ser Phe
755 760 765

Asp Phe Lys Gly Ala Lys Leu Ile Leu Glu Thr Val Lys Glu Asp Ser
770 775 780

Lys Glu Arg Arg Asp Ser Arg Ala Arg Glu Lys His Pro Ala Arg
785 790 795 800

Glu Lys Glu Lys Pro Asp Lys Arg Lys Arg Tyr Lys Glu Lys Asp Lys
805 810 815

Asp Lys Ser Glu Lys Ser Ile Leu Glu Lys Cys Gln Lys Asp Lys Glu
820 825 830

Lys Lys Glu Lys His Lys Asp Thr His Gly Lys Asp Lys Glu Arg Lys
835 840 845

Ala Ser Val Phe Glu Lys His Lys Glu Lys Lys Asp Lys Glu Ser Thr
850 855 860

Glu Lys Tyr Lys Asp Arg Ala Ser Val Asp Ser Thr Gln Asp Lys Lys
865 870 875 880

Asn Lys Gln Glu Lys Ala Glu Lys Lys His Ala Ala Glu Asp Lys Ala
885 890 895

Lys Ser Lys His Lys Glu Lys Ser Asp Lys Glu His Ser Lys Glu Arg
900 905 910

Lys Ser Ser Arg Ser Ala Asp Ala Glu Tyr Arg Glu Ser Glu Val Ser
915 920 925

Ser Asp Ser Phe Thr Asp Arg Glu Asp Asp Lys Ser Ala Cys Leu Pro
930 935 940

Glu Lys Leu Lys Glu Lys Arg His Arg His Ser Ser Ser Ser Lys
945 950 955 960

Lys Ser His Asp Arg Glu Glu Lys Lys Glu Asp Tyr Lys Glu Gly Arg
965 970 975

Lys Gly Gln Tyr Glu Lys Asp Leu Glu Ala Asp Ala Tyr Gly Val Ser
980 985 990

Tyr Asn Met Lys Ala Ile Glu Leu Phe Glu Lys Iys Asp Lys Asn Asp
995 1000 1005

Glu Pro Leu Lys Glu Lys Lys Arg Glu Lys His Arg Glu Lys Trp
1010 1015 1020

Arg Asp Glu Lys Glu Arg His Arg Asp Arg His Ala Asp Arg Pro Lys
1025 1030 1035 1040

Pro Ser Lys Asp Pro Gly Lys Lys Asp Ala Arg Pro Arg Glu Lys Leu
1045 1050 1055

Leu Gly Asp Gly Asp Leu Met Met Thr Ser Phe Glu Arg Met Leu Ser
1060 1065 1070

Gln Lys Asp Leu Glu Ile Glu Glu Arg His Lys Arg His Lys Glu Arg
1075 1080 1085

Met Lys Gln Met Glu Lys Leu Arg His Arg Ser Gly Asp Pro Lys Leu
1090 1095 1100

Lys Glu Lys Ala Lys Pro Ala Asp Asp Gly Arg Lys Lys Gly Leu Asp
1105 1110 1115 1120

Ile Pro Ala Lys Lys Pro Pro Gly Leu Asp Pro Pro Phe Lys Asp Lys		
1125	1130	1135
Lys Leu Lys Glu Ser Thr Pro Ile Pro Pro Ala Ala Glu Asn Lys Leu		
1140	1145	1150
His Pro Ala Ser Gly Ala Asp Ser Lys Asp Trp Leu Ala Gly Pro His		
1155	1160	1165
Met Lys Glu Val Leu Pro Ala Ser Pro Arg Pro Asp Gln Ser Arg Pro		
1170	1175	1180
Thr Gly Val Pro Thr Pro Thr Ser Val Leu Ser Cys Pro Ser Tyr Glu		
1185	1190	1195
Glu Val Met His Thr Pro Arg Thr Pro Ser Cys Ser Ala Asp Asp Tyr		
1205	1210	1215
Ala Asp Leu Val Phe Asp Cys Ala Asp Ser Gln His Ser Thr Pro Val		
1220	1225	1230
Pro Thr Ala Pro Thr Ser Ala Cys Ser Pro Ser Phe Phe Asp Arg Phe		
1235	1240	1245
Ser Val Ala Ser Ser Gly Leu Ser Glu Asn Ala Ser Gln Ala Pro Ala		
1250	1255	1260
Arg Pro Leu Ser Thr Asn Leu Tyr Arg Ser Val Ser Val Asp Ile Asp		
1265	1270	1275
Lys Leu Phe Arg Gln Gln Ser Val Pro Ala Ala Ser Ser Tyr Asp Ser		
1285	1290	1295
Pro Met Pro Pro Ser Met Glu Asp Arg Ala Pro Leu Pro Pro Val Pro		
1300	1305	1310
Ala Glu Lys Phe Ala Cys Leu Ser Pro Gly Tyr Tyr Ser Pro Asp Tyr		
1315	1320	1325
Gly Leu Pro Ser Pro Lys Val Asp Ala Leu His Cys Pro Pro Ala Ala		
1330	1335	1340
Val Val Thr Val Thr Pro Ser Pro Glu Gly Val Phe Ser Ser Leu Gln		
1345	1350	1355
Ala Lys Pro Ser Pro Ser Pro Pro Ser Leu Asp Thr Ser Glu Asp Gln		
1365	1370	1375

Gln Ala Thr Ala Ala Ile Ile Pro Pro Glu Pro Ser Tyr Leu Glu Pro
 1380 1385 1390

 Leu Asp Glu Gly Pro Phe Ser Ala Val Ile Thr Glu Glu Pro Val Glu
 1395 1400 1405

 Trp Ala His Pro Ser Glu Gln Ala Leu Ala Ser Ser Leu Ile Gly Gly
 1410 1415 1420

 Thr Ser Glu Asn Pro Val Ser Trp Pro Val Gly Ser Asp Leu Leu Leu
 1425 1430 1435 1440

 Lys Ser Pro Gln Arg Phe Pro Glu Ser Pro Lys Arg Phe Cys Pro Ala
 1445 1450 1455

 Asp Pro Leu His Ser Ala Ala Pro Gly Pro Phe Ser Ala Ser Glu Ala
 1460 1465 1470

 Pro Tyr Pro Ala Pro Pro Ala Ser Pro Ala Pro Tyr Ala Leu Pro Val
 1475 1480 1485

 Ala Glu Leu Glu Asp Val Lys Asp Val Pro Ala Ala Ile Ser Thr Ser
 1490 1495 1500

 Glu Ala Ala Pro Tyr Ala Pro Pro Ser Gly Leu Glu Ser Phe Phe Ser
 1505 1510 1515 1520

 Asn Cys Lys Ser Leu Pro Glu Ala Pro Leu Asp Val Ala Pro Glu Ala
 1525 1530 1535

 Leu Gly Pro Leu Glu Asn Ser Phe Leu Asp Gly Ser Arg Gly Leu Ser
 1540 1545 1550

 His Leu Gly Gln Val Glu Pro Val Pro Trp Ala Asp Ala Phe Ala Gly
 1555 1560 1565

 Pro Glu Asp Asp Leu Asp Leu Gly Pro Phe Ser Leu Pro Glu Leu Pro
 1570 1575 1580

 Leu Gln Thr Lys Asp Ala Ala Asp Gly Glu Ala Glu Pro Val Glu Glu
 1585 1590 1595 1600

 Ser Leu Ala Pro Pro Glu Glu Met Pro Pro Gly Ala Pro Arg Glu Leu
 1605 1610 1615

 Glu Pro Glu Pro Ser Gly Glu Pro Lys Leu Asp Val Ala Leu Glu Ala
 1620 1625 1630

Ala Val Glu Ala Glu Thr Val Pro Glu Glu Arg Ala Arg Gly Asp Pro
 1635 1640 1645

 Asp Ser Ser Val Glu Pro Ala Pro Val Pro Pro Glu Gln Leu Gly Ser
 1650 1655 1660

 Gly Asp Pro Ser Leu Cys Ala Pro Asp Gly Pro Ala Pro Asn Thr Val
 1665 1670 1675 1680

 Ala Gln Ala Gln Ala Ala Asp Gly Ala Gly Pro Glu Asp Asp Thr Glu
 1685 1690 1695

 Ala Ser Arg Ala Ala Ala Pro Ala Glu Gly Pro Pro Gly Gln Pro Glu
 1700 1705 1710

 Ala Ala Glu Pro Lys Pro Thr Ala Glu Ala Pro Lys Ala Pro Arg Glu
 1715 1720 1725

 Ile Pro Gln Arg Met Thr Arg Asn Arg Ala Gln Met Leu Ala Asn Gln
 1730 1735 1740

 Ser Lys Gln Gly Pro Pro Pro Ser Glu Lys Glu Cys Ala Pro Thr Pro
 1745 1750 1755 1760

 Ala Pro Val Thr Arg Ala Lys Ala Arg Gly Ser Glu Asp Asp Asp Ala
 1765 1770 1775

 Gln Ala Gln His Pro Arg Lys Arg Arg Phe Gln Arg Ser Thr Gln Gln
 1780 1785 1790

 Leu Gln Leu Asn Thr Ser Thr Gln Gln Thr Arg Glu Val Ile Gln Gln
 1795 1800 1805

 Thr Leu Ala Ala Ile Val Asp Ala Ile Lys Leu Asp Ala Ile Glu Pro
 1810 1815 1820

 Tyr His Ser Asp Arg Ala Asn Pro Tyr Phe Glu Tyr Leu Gln Ile Arg
 1825 1830 1835 1840

 Lys Lys Ile Glu Glu Lys Arg Lys Ile Leu Cys Cys Ile Thr Pro Gln
 1845 1850 1855

 Ala Pro Gln Cys Tyr Ala Glu Tyr Val Thr Tyr Thr Gly Ser Tyr Leu
 1860 1865 1870

 Leu Asp Gly Lys Pro Leu Ser Lys Leu His Ile Pro Val Ile Ala Pro
 1875 1880 1885

Pro Pro Ser Leu Ala Glu Pro Leu Lys Glu Leu Phe Arg Gln Gln Glu
1890 1895 1900

Ala Val Arg Gly Lys Leu Arg Leu Gln His Ser Ile Glu Arg Glu Lys
1905 1910 1915 1920

Leu Ile Val Ser Cys Glu Gln Glu Ile Leu Arg Val His Cys Arg Ala
1925 1930 1935

Ala Arg Thr Ile Ala Asn Gln Ala Val Pro Phe Ser Ala Cys Thr Met
1940 1945 1950

Leu Leu Asp Ser Glu Val Tyr Asn Met Pro Leu Glu Ser Gln Gly Asp
1955 1960 1965

Glu Asn Lys Ser Val Arg Asp Arg Phe Asn Ala Arg Gln Phe Ile Ser
1970 1975 1980

Trp Leu Gln Asp Val Asp Asp Lys Tyr Asp Arg Met Lys Val Cys Leu
1985 1990 1995 2000

Leu Met Arg Gln Gln His Glu Ala Ala Ala Leu Asn Ala Val Gln Arg
2005 2010 2015

Met Glu Trp Gln Leu Lys Val Gln Glu Leu Asp Pro Ala Gly His Lys
2020 2025 2030

Ser Leu Cys Val Asn Glu Val Pro Ser Phe Tyr Val Pro Met Val Asp
2035 2040 2045

Val Asn Asp Asp Phe Val Leu Leu Pro Ala
2050 2055

<210> 21

<211> 1749

<212> DNA

<213> Homo sapiens

<400> 21

agaacgcgga gagtcgcccgc ctggccgggc gtagacgcgg tggcagagcc cgcgcggcgc 60
tggaaagcgag tggcggagcg gcgggacctc ggccgactcg ccatggagga ggagggtgtg 120
aaggaagccg gtgagaagcc tcggggagca cagatggtg acaaggctgg ctggatcaag 180
aagagcagtg gggccctcct gggttctgg aaagaccat atctgctcct ctgccaggcc 240
cagctgctgg tctatgagaa tgaggatgt cagaagtgtg tggagactgt ggagctggc 300
agctatgaga agtgcgcagga ctttcgtgcc ctccctcaagc gaaaacaccg ctttatcctg 360
ctgcgcattcc cagggAACAA ggtcagcgcac atcaaattcc aggcaccac cggggaggag 420
aaggaatcct ggatcaaagc cctcaatgaa gggattaacc gaggcaaaaa caaggctttc 480

gatgaggtaa aggtggacaa gagctgcgcc ctggagcatg tgacacggga ccgggtgcga 540
 gggggccagc gacgccggcc accaacgaga gtccacctga aggaggtggc cagtgcagct 600
 tctgacggtc ttctgcgcct gnatcttgcat gttccggaca gtggggccacc agtgtttgcc 660
 cccagcaatc atgtcagtga agcccaacct cggagacac cccggccct catgcctcct 720
 accaagcctt tccttagcacc tgagaccacc agccctggta acaggggtgga gaccctgtg 780
 ggggagagag ccccaacccc tgtctcagca agctctgagg tctccctga gagccaagag 840
 gactcagaga cccccagcaga ggaggacagt ggctctgagc agcctccaa cagcgtcctg 900
 cctgacaaac tgaaggtgag ctgggagaac cccagccccc aggagggccc tgctgcagag 960
 agtgcagaac cgtcccaggc accctgtct gagacttctg aggctgcccc cagggagggt 1020
 gggaaagcccc ctacacccccc acccaagatc ttatcagaag aacactgaa agcctccatg 1080
 ggtgagatgc aggcttctgg gccacctgct ccaggcacag tgaaaggctc cagtcaaatg 1140
 gcaagaatgg aaggactgag cattgccaag cactctaagg ctgaaggcac ccaaagaact 1200
 tctccaaagg atgcactaac acaccaagca ctgccccct gggacctgccc acctcagttc 1260
 catcaccgct gctcctccct tggggacttg ctggggaaag gcccgcggca tcccttgca 1320
 cccaggcaac ggctatatatcg ggcccagctg gaggtgaagg tggctcgga acagacggag 1380
 aaactgttga acaaggtgct gggcagtgag ccggccctg ttagtggca aacattgctc 1440
 agccaggctg tggagcagct gaggcagggcc acccaggtcc tgcagggaaat gagagattg 1500
 ggagagctga gccaggaagc acctgggcta agggagaagc ggaaggagct ggtgaccctc 1560
 tacaggagaa gtgcacccta gggccttctg ggcagagggc accatccctt ctggccatcc 1620
 atcaagtcca tcaaggccca gcccgtctga gaaatgtct tctgcttcta cagcaatggc 1680
 tgcaggaggg ccattggca tgtcagggtt tggccatgac ccgaagagac tcctggcggtc 1740
 cttcctact 1749

<210> 22
 <211> 492
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Glu Glu Glu Gly Val Lys Glu Ala Gly Glu Lys Pro Arg Gly Ala
 1 5 10 15

Gln Met Val Asp Lys Ala Gly Trp Ile Lys Lys Ser Ser Gly Gly Leu
 20 25 30

Leu Gly Phe Trp Lys Asp Arg Tyr Leu Leu Leu Cys Gln Ala Gln Leu
 35 40 45

Leu Val Tyr Glu Asn Glu Asp Asp Gln Lys Cys Val Glu Thr Val Glu
 50 55 60

Leu Gly Ser Tyr Glu Lys Cys Gln Asp Leu Arg Ala Leu Leu Lys Arg
 65 70 75 80

Lys His Arg Phe Ile Leu Leu Arg Ser Pro Gly Asn Lys Val Ser Asp
 85 90 95

Ile Lys Phe Gln Ala Pro Thr Gly Glu Glu Lys Ser Trp Ile Lys
100 105 110

Ala Leu Asn Glu Gly Ile Asn Arg Gly Lys Asn Lys Ala Phe Asp Glu
115 120 125

Val Lys Val Asp Lys Ser Cys Ala Leu Glu His Val Thr Arg Asp Arg
130 135 140

Val Arg Gly Gly Gln Arg Arg Arg Pro Pro Thr Arg Val His Leu Lys
145 150 155 160

Glu Val Ala Ser Ala Ala Ser Asp Gly Leu Leu Arg Leu Asp Leu Asp
165 170 175

Val Pro Asp Ser Gly Pro Pro Val Phe Ala Pro Ser Asn His Val Ser
180 185 190

Glu Ala Gln Pro Arg Glu Thr Pro Arg Pro Leu Met Pro Pro Thr Lys
195 200 205

Pro Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly Asp Arg Val Glu Thr
210 215 220

Pro Val Gly Glu Arg Ala Pro Thr Pro Val Ser Ala Ser Ser Glu Val
225 230 235 240

Ser Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro Ala Glu Glu Asp Ser
245 250 255

Gly Ser Glu Gln Pro Pro Asn Ser Val Leu Pro Asp Lys Leu Lys Val
260 265 270

Ser Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro Ala Glu Ser Ala
275 280 285

Glu Pro Ser Gln Ala Pro Cys Ser Glu Thr Ser Glu Ala Ala Pro Arg
290 295 300

Glu Gly Gly Lys Pro Pro Thr Pro Pro Pro Lys Ile Leu Ser Glu Glu
305 310 315 320

His Leu Lys Ala Ser Met Gly Glu Met Gln Ala Ser Gly Pro Pro Ala
325 330 335

Pro Gly Thr Val Lys Gly Leu Ser Gln Met Ala Arg Met Glu Gly Leu
340 345 350

Ser Ile Ala Lys His Ser Lys Ala Glu Gly Thr Gln Arg Thr Ser Pro
355 360 365

Lys Asp Ala Leu Thr His Gln Ala Leu Pro Pro Trp Asp Leu Pro Pro
370 375 380

Gln Phe His His Arg Cys Ser Ser Leu Gly Asp Leu Leu Gly Glu Gly
385 390 395 400

Pro Arg His Pro Leu Gln Pro Arg Gln Arg Leu Tyr Arg Ala Gln Leu
405 410 415

Glu Val Lys Val Ala Ser Glu Gln Thr Glu Lys Leu Leu Asn Lys Val
420 425 430

Leu Gly Ser Glu Pro Ala Pro Val Ser Ala Glu Thr Leu Leu Ser Gln
435 440 445

Ala Val Glu Gln Leu Arg Gln Ala Thr Gln Val Leu Gln Glu Met Arg
450 455 460

Asp Leu Gly Glu Leu Ser Gln Glu Ala Pro Gly Leu Arg Glu Lys Arg
465 470 475 480

Lys Glu Leu Val Thr Leu Tyr Arg Arg Ser Ala Pro
485 490

<210> 23

<211> 1491

<212> DNA

<213> Homo sapiens

<400> 23

ggggccgcgc agccccggcc ggaacccacc atgcggcggc tgcggcgccct ggcgcaccc 60
gtgctttctt gccccttctc caagcgcctg caggccggc tcccaggcct cagggtccgc 120
tgcattttcc tggcctggct gggcgtctt gcaggcagct ggctgggtta cgtgcactac 180
tcgtcctact cggagcgctg tcgcggccat gtctgccagg tggtcatttg tgaccagttac 240
cgcaaggggta tcatctcggt ctccgtctgc cagcacctgt gtgagctgca tatgggtggag 300
tggaggacct gcctctcggt ggccccgggc cagcagggtgt acagcgggct ctggcgggac 360
aaggatgtaa ccatcaagtg tggcatttag gagaccctcg actccaaggc ccggtcggat 420
gcggccccc ggcgggagct ggtactgtt gacaagccca cccggggcac ctccatcaag 480
gaattccggg agatgaccct cggcttcctc aaggcgaacc tgggagacct gccttccctg 540
ccggcgctgg ttggccaggt cctgctcatg gctgacttca acaaggacaa ccgggtgtcc 600
ctggcggaag ccaagtccgt gtggccctg ctgcagcgta acgagttcct gctgctgctg 660
tccctgcagg agaaggagca cgcctccaga ctgctgggtct actgtgggaa cctctacctc 720
accgagggcg tgccgcatgg cgcctggcac gcggccgccc ttccacccct gttgcgccc 780
ctgctgccgc ctgcccctgca gggtgctctc cagcagtggc tggggccctgc gtggccttgg 840

cgggccaaga tcgcccattcg cctgctggag ttctgtggagg agctcttcca cggctttac 900
gggactttct acatgtgtga gaccacactg gccaacgtgg gctacacagc cacctacgac 960
ttcaagatgg ccgacactgca gcaggtggca cccgaggcca ccgtgcgccc cttccctgcag 1020
ggccgcccgtc gcgagcacag caccgactgc acctacgggc gcgactgcag ggccccgtgt 1080
gacaggctca tgagggcgtg caagggcgtac ctcatccagc ccaacctggc caaggtgtgc 1140
gcactgctac ggggctaccc gctgcctggc gcgcccggc acctccgcga ggagctggc 1200
acacagctgc gcacactgtac cacgctgagc gggctggcca gccaggtgga ggcccatcac 1260
tcgctgggtgc tcagccaccc caagactctg ctctggaaaga agatctccaa caccaagtac 1320
tcttgatggg gcagtgaggg gcctggccac ccttcctggc gctggccagg tgccagggtc 1380
caaccctccc tcaaggagag tcctccaagg gggttgtta ctctgaagaa cgtaatgtca 1440
ataaacagct tttatgtaaat gcccaggctc gaggcaccctg agccccatc a 1491

<210> 24

<211> 431

<212> PRT

<213> Homo sapiens

<400> 24

Met Arg Arg Leu Arg Arg Leu Ala His Leu Val Leu Phe Cys Pro Phe
1 5 10 15

Ser Lys Arg Leu Gln Gly Arg Leu Pro Gly Leu Arg Val Arg Cys Ile
20 25 30

Phe Leu Ala Trp Leu Gly Val Phe Ala Gly Ser Trp Leu Val Tyr Val
35 40 45

His Tyr Ser Ser Tyr Ser Glu Arg Cys Arg Gly His Val Cys Gln Val
50 55 60

Val Ile Cys Asp Gln Tyr Arg Lys Gly Ile Ile Ser Gly Ser Val Cys
65 70 75 80

Gln Asp Leu Cys Glu Leu His Met Val Glu Trp Arg Thr Cys Leu Ser
85 90 95

Val Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp Arg Asp Lys Asp
100 105 110

Val Thr Ile Lys Cys Gly Ile Glu Glu Thr Leu Asp Ser Lys Ala Arg
115 120 125

Ser Asp Ala Ala Pro Arg Arg Glu Leu Val Leu Phe Asp Lys Pro Thr
130 135 140

Arg Gly Thr Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Gly Phe Leu
145 150 155 160

Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu Val Gly Gln
165 170 175

Val Leu Leu Met Ala Asp Phe Asn Lys Asp Asn Arg Val Ser Leu Ala
180 185 190

Glu Ala Lys Ser Val Trp Ala Leu Leu Gln Arg Asn Glu Phe Leu Leu
195 200 205

Leu Leu Ser Leu Gln Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr
210 215 220

Cys Gly Asp Leu Tyr Leu Thr Glu Gly Val Pro His Gly Ala Trp His
225 230 235 240

Ala Ala Ala Leu Pro Pro Leu Leu Arg Pro Leu Leu Pro Pro Ala Leu
245 250 255

Gln Gly Ala Leu Gln Gln Trp Leu Gly Pro Ala Trp Pro Trp Arg Ala
260 265 270

Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly
275 280 285

Ser Tyr Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val Gly
290 295 300

Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu Gln Gln Val Ala
305 310 315 320

Pro Glu Ala Thr Val Arg Arg Phe Leu Gln Gly Arg Arg Cys Glu His
325 330 335

Ser Thr Asp Cys Thr Tyr Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg
340 345 350

Leu Met Arg Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys
355 360 365

Val Cys Ala Leu Leu Arg Gly Tyr Leu Leu Pro Gly Ala Pro Ala Asp
370 375 380

Leu Arg Glu Glu Leu Gly Thr Gln Leu Arg Thr Cys Thr Thr Leu Ser
385 390 395 400

Gly Leu Ala Ser Gln Val Glu Ala His His Ser Leu Val Leu Ser His
405 410 415

Leu Lys Thr Leu Leu Trp Lys Lys Ile Ser Asn Thr Lys Tyr Ser
420 425 430

<210> 25
<211> 1062
<212> DNA
<213> Homo sapiens

<400> 25
tagagatgga tggaaccaat ggcagcaccc aaacccattt catcctactg ggattctctg 60
accgacccca tctggagagg atcctcttg tggcatcct gatcgctac ctcctgaccc 120
tcgttagccaa caccaccatc atcctgggt cccggctgga ccccccaccc cacaccccca 180
tgtacttctt cctcgccac ctttccttcc tggacctcag tttcaccacc agtccatcc 240
cccagctgct ctacaacctt aatggatgtg acaagaccat cagctacatg ggctgtgcca 300
tccagcttctt cctgttcctg ggtctgggt gtgtggagtg cctgcttctg gctgtcatgg 360
cctatgaccg gtgtgtggct atctgcaagc ccctgcacta catggtgatc atgaacccca 420
ggctctgccc gggcttggtg tcagtgcacct gggctgtgg ggtggccaac tccttgcca 480
tgtctctgt gaccctgcgc ttaccccgct gtgggcacca cgaggtggac cacttcctgc 540
gtgagatgcc cgcctgtatc cggatggct gcgtcagcac tggccatc gaaggcaccg 600
tctttgtcct gaaaaaaaggt gttgtgtgtt ccccttggt gtttatcttctg ctctcttaca 660
gctacattgt gagggtgtg ttacaaattt ggtcagcatc aggaaggcag aaggccttcg 720
gcacctgcgg ctcccatctc actgtggctt ccctttctt tggaaacatc atctacatgt 780
acatgcagcc aggagccagt tttcccaagg accagggcat gttcctcatg ctctcttaca 840
acattgtcac ccccttcctc aatcctctca tctacaccct cagaaacaga gaggtgaagg 900
gggcactggg aagggttgctt ctggggaaaga gagagctagg aaaggagtaa aggcattcc 960
acctgacttc acttccatcc agggccactg gcagcatctg gaacggctga attccagctg 1020
atattagcccc acgactccca acttgccttt ttctggactt tt 1062

<210> 26
<211> 314
<212> PRT
<213> Homo sapiens

<400> 26
Met Asp Gly Thr Asn Gly Ser Thr Gln Thr His Phe Ile Leu Leu Gly
1 5 10 15

Phe Ser Asp Arg Pro His Leu Glu Arg Ile Leu Phe Val Val Ile Leu
20 25 30

Ile Ala Tyr Leu Leu Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val
35 40 45

Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
50 55 60

His	Leu	Ser	Phe	Leu	Asp	Leu	Ser	Phe	Thr	Thr	Ser	Ser	Ile	Pro	Gln
65				70					75					80	
Leu	Leu	Tyr	Asn	Leu	Asn	Gly	Cys	Asp	Lys	Thr	Ile	Ser	Tyr	Met	Gly
			85					90					95		
Cys	Ala	Ile	Gln	Leu	Phe	Leu	Phe	Leu	Gly	Leu	Gly	Gly	Val	Glu	Cys
			100					105					110		
Leu	Leu	Leu	Ala	Val	Met	Ala	Tyr	Asp	Arg	Cys	Val	Ala	Ile	Cys	Lys
			115				120					125			
Pro	Leu	His	Tyr	Met	Val	Ile	Met	Asn	Pro	Arg	Leu	Cys	Arg	Gly	Leu
			130				135				140				
Val	Ser	Val	Thr	Trp	Gly	Cys	Gly	Val	Ala	Asn	Ser	Leu	Ala	Met	Ser
	145			150				155					160		
Pro	Val	Thr	Leu	Arg	Leu	Pro	Arg	Cys	Gly	His	His	Glu	Val	Asp	His
	165					170						175			
Phe	Leu	Arg	Glu	Met	Pro	Ala	Leu	Ile	Arg	Met	Ala	Cys	Val	Ser	Thr
	180					185					190				
Val	Ala	Ile	Glu	Gly	Thr	Val	Phe	Val	Leu	Lys	Lys	Gly	Val	Val	Leu
	195					200				205					
Ser	Pro	Leu	Val	Phe	Ile	Leu	Leu	Ser	Tyr	Ser	Tyr	Ile	Val	Arg	Ala
	210					215				220					
Val	Leu	Gln	Ile	Arg	Ser	Ala	Ser	Gly	Arg	Gln	Lys	Ala	Phe	Gly	Thr
	225			230				235					240		
Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ser	Leu	Phe	Tyr	Gly	Asn	Ile	Ile
	245					250						255			
Tyr	Met	Tyr	Met	Gln	Pro	Gly	Ala	Ser	Ser	Ser	Gln	Asp	Gln	Gly	Met
	260					265					270				
Phe	Leu	Met	Leu	Phe	Tyr	Asn	Ile	Val	Thr	Pro	Leu	Leu	Asn	Pro	Leu
	275					280					285				
Ile	Tyr	Thr	Leu	Arg	Asn	Arg	Glu	Val	Lys	Gly	Ala	Leu	Gly	Arg	Leu
	290					295				300					
Leu	Leu	Gly	Lys	Arg	Glu	Leu	Gly	Lys	Glu						
	305				310										

<210> 27
<211> 1062
<212> DNA
<213> Homo sapiens

<400> 27
tagagatgga tggaaccaat ggacgcaccc aaacccattt catcctactg ggattctctg 60
accgacccca tctggagagg atcctcttg tggcatcct gatcgctac ctcctgaccc 120
tcgtaggcaa caccaccatc atcctgggt cccggctgga ccccccaccc cacaccccca 180
tgtacttctt cctcgccac ctttccttcc tggacctcag tttcaccacc agtcctatcc 240
cccagctgct ctacaacctt aatggatgtg acaagaccat cagctacatg ggctgtgcca 300
tccagcttt cctgttcctg ggtctgggt gtgtggagtg cctgcttctg gctgtcatgg 360
cctatgaccg gtgtgtggct atctgcaagc ccctgcacta catggatgatc atgaacccca 420
ggctctgccc gggcttgggt tcagtgcactt gggctgtgg ggtggccaac tccttggcca 480
tgtctccgtt gaccctgcgc ttaccccgct gtgggcacca cgaggtggac cacttcctgc 540
gtgagatgcc cgcctgtatc cggatggct gcgtcagcac tggccatc gacggcaccg 600
tctttgtcctt ggcgggtgggt gttgtgtgtt ccccttgggt gtttatcctg ctctcttaca 660
gttacattgtt gagggtgtgtt ttacaaattt ggtcagcata aggaaggcag aaggecttcg 720
gcacctgcgg ctcccatctc actgtggctt ccctttcta tggaaacatc atttacatgt 780
acatgcagcc aggagccagt tttcccaagg accagggcat gttcctcatg ctcttcttaca 840
acattgtcac ccccttcctc aatcctctca tctacaccctt cagaaacaga gaggtgaagg 900
gggcactggg aaggttgtt ttggggaaaga gagagctagg aaaggagtaa aggcatctcc 960
acctgacttc acttccatcc agggccactg gcagcatctg gaacggctga attccagctg 1020
atattagccc acgactccca acttgccttt ttctggactt tt 1062

<210> 28
<211> 314
<212> PRT
<213> Homo sapiens

<400> 28
Met Asp Gly Thr Asn Gly Ser Thr Gln Thr His Phe Ile Leu Leu Gly
1 5 10 15
Phe Ser Asp Arg Pro His Leu Glu Arg Ile Leu Phe Val Val Ile Leu
20 25 30
Ile Ala Tyr Leu Leu Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val
35 40 45
Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
50 55 60
His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro Gln
65 70 75 80

Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met Gly
85 90 95

Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu Cys
100 105 110

Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys Lys
115 120 125

Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly Leu
130 135 140

Val Ser Val Thr Trp Gly Cys Gly Val Ala Asn Ser Leu Ala Met Ser
145 150 155 160

Pro Val Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp His
165 170 175

Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser Thr
180 185 190

Val Ala Ile Asp Gly Thr Val Phe Val Leu Ala Val Gly Val Val Leu
195 200 205

Ser Pro Leu Val Phe Ile Leu Ser Tyr Ser Tyr Ile Val Arg Ala
210 215 220

Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly Thr
225 230 235 240

Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile
245 250 255

Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly Met
260 265 270

Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro Leu
275 280 285

Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg Leu
290 295 300

Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu
305 310

<211> 624

<212> DNA

<213> Homo sapiens

<400> 29

ctttgagctt ctctgactgc tgaccactga cccaccgact tcatgacagc accctcggt 60
gccttccag ttcaaattccg gcagccctca gtcagcggcc tctcgagat aaccaaaagc 120
ctgtatatac gcaatggtgt ggccgccaac aacaagctca tgctgtctag caaccagatc 180
accatggta tcaatgtctc agtggaggt a gtgaacaccc tttatgagga tatccagttac 240
atgcaggta ctgtggctga ctccccta ac tcacgtctt gtgacttctt tgaccctatt 300
gctgaccata tccacacggt ggagatgaag cagggccgt a ctttgctgca ctgtgtgt 360
ggtgtgagcc gctcagctgc cctgtgcctc gcctacactca tgaagtacca cgccatgtcc 420
ctgctggacg cccacacgtg gaccaagtca tgccggccca tcatccgacc caacagcgcc 480
ttttgggagc agctcatcca ctatgagtttca aattgtttt gcaagaacac tttgcacatg 540
gtcagttccc cagtggaat gatccctgac atctatgaga aggaagtccg tttgtatgatt 600
ccactgtgag ccatcccacg agcc 624

<210> 30

<211> 188

<212> PRT

<213> Homo sapiens

<400> 30

Met Thr Ala Pro Ser Cys Ala Phe Pro Val Gln Ile Arg Gln Pro Ser
1 5 10 15

Val Ser Gly Leu Ser Gln Ile Thr Lys Ser Leu Tyr Ile Ser Asn Gly
20 25 30

Val Ala Ala Asn Asn Lys Leu Met Leu Ser Ser Asn Gln Ile Thr Met
35 40 45

Val Ile Asn Val Ser Val Glu Val Val Asn Thr Leu Tyr Glu Asp Ile
50 55 60

Gln Tyr Met Gln Val Pro Val Ala Asp Ser Pro Asn Ser Arg Leu Cys
65 70 75 80

Asp Phe Phe Asp Pro Ile Ala Asp His Ile His Ser Val Glu Met Lys
85 90 95

Gln Gly Arg Thr Leu Leu His Cys Ala Ala Gly Val Ser Arg Ser Ala
100 105 110

Ala Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ala Met Ser Leu Leu
115 120 125

Asp Ala His Thr Trp Thr Lys Ser Cys Arg Pro Ile Ile Arg Pro Asn
130 135 140

Ser Gly Phe Trp Glu Gln Leu Ile His Tyr Glu Phe Gln Leu Phe Gly
145 150 155 160

Lys Asn Thr Val His Met Val Ser Ser Pro Val Gly Met Ile Pro Asp
165 170 175

Ile Tyr Glu Lys Glu Val Arg Leu Met Ile Pro Leu
180 185

<210> 31

<211> 1034

<212> PRT

<213> Mus musculus

<400> 31

Met Pro Leu Cys Pro Leu Leu Leu Leu Ala Leu Gly Leu Arg Leu Thr
1 5 10 15

Gly Thr Leu Asn Ser Asn Asp Pro Asn Val Cys Thr Phe Trp Glu Ser
20 25 30

Phe Thr Thr Thr Lys Glu Ser His Leu Arg Pro Phe Ser Leu Leu
35 40 45

Pro Ala Glu Ser Cys His Arg Pro Trp Glu Asp Pro His Thr Cys Ala
50 55 60

Gln Pro Thr Val Val Tyr Arg Thr Val Tyr Arg Gln Val Val Lys Met
65 70 75 80

Asp Ser Arg Pro Arg Leu Gln Cys Cys Arg Gly Tyr Tyr Glu Ser Arg
85 90 95

Gly Ala Cys Val Pro Leu Cys Ala Gln Glu Cys Val His Gly Arg Cys
100 105 110

Val Ala Pro Asn Gln Cys Gln Cys Ala Pro Gly Trp Arg Gly Gly Asp
115 120 125

Cys Ser Ser Glu Cys Ala Pro Gly Met Trp Gly Pro Gln Cys Asp Lys
130 135 140

Phe Cys His Cys Gly Asn Asn Ser Ser Cys Asp Pro Lys Ser Gly Ala
145 150 155 160

Cys Phe Cys Pro Ser Gly Leu Gln Pro Pro Asn Cys Leu Gln Pro Cys
 165 170 175

 Pro Ala Gly His Tyr Gly Pro Ala Cys Gln Phe Asp Cys Gln Cys Tyr
 180 185 190

 Gly Ala Ser Cys Asp Pro Gln Asp Gly Ala Cys Phe Cys Pro Pro Gly
 195 200 205

 Arg Ala Gly Pro Ser Cys Asn Val Pro Cys Ser Gln Gly Thr Asp Gly
 210 215 220

 Phe Phe Cys Pro Arg Thr Tyr Pro Cys Gln Asn Gly Gly Val Pro Gln
 225 230 235 240

 Gly Ser Gln Gly Ser Cys Ser Cys Pro Pro Gly Trp Met Gly Val Ile
 245 250 255

 Cys Ser Leu Pro Cys Pro Glu Gly Phe His Gly Pro Asn Cys Thr Gln
 260 265 270

 Glu Cys Arg Cys His Asn Gly Gly Leu Cys Asp Arg Phe Thr Gly Gln
 275 280 285

 Cys His Cys Ala Pro Gly Tyr Ile Gly Asp Arg Cys Gln Glu Glu Cys
 290 295 300

 Pro Val Gly Arg Phe Gly Gln Asp Cys Ala Glu Thr Cys Asp Cys Ala
 305 310 315 320

 Pro Gly Ala Arg Cys Phe Pro Ala Asn Gly Ala Cys Leu Cys Glu His
 325 330 335

 Gly Phe Thr Gly Asp Arg Cys Thr Glu Arg Leu Cys Pro Asp Gly Arg
 340 345 350

 Tyr Gly Leu Ser Cys Gln Glu Pro Cys Thr Cys Asp Pro Glu His Ser
 355 360 365

 Leu Ser Cys His Pro Met His Gly Glu Cys Ser Cys Gln Pro Gly Trp
 370 375 380

 Ala Gly Leu His Cys Asn Glu Ser Cys Pro Gln Asp Thr His Gly Pro
 385 390 395 400

 Gly Cys Gln Glu His Cys Leu Cys Leu His Gly Gly Leu Cys Leu Ala
 405 410 415

Asp Ser Gly Leu Cys Arg Cys Ala Pro Gly Tyr Thr Gly Pro His Cys
420 425 430

Ala Asn Leu Cys Pro Pro Asp Thr Tyr Gly Ile Asn Cys Ser Ser Arg
435 440 445

Cys Ser Cys Glu Asn Ala Ile Ala Cys Ser Pro Ile Asp Gly Thr Cys
450 455 460

Ile Cys Lys Glu Gly Trp Gln Arg Gly Asn Cys Ser Val Pro Cys Pro
465 470 475 480

Leu Gly Thr Trp Gly Phe Asn Cys Asn Ala Ser Cys Gln Cys Ala His
485 490 495

Asp Gly Val Cys Ser Pro Gln Thr Gly Ala Cys Thr Cys Thr Pro Gly
500 505 510

Trp His Gly Ala His Cys Gln Leu Pro Cys Pro Lys Gly Gln Phe Gly
515 520 525

Glu Gly Cys Ala Ser Val Cys Asp Cys Asp His Ser Asp Gly Cys Asp
530 535 540

Pro Val His Gly Gln Cys Arg Cys Gln Ala Gly Trp Met Gly Thr Arg
545 550 555 560

Cys His Leu Pro Cys Pro Glu Gly Phe Trp Gly Ala Asn Cys Ser Asn
565 570 575

Thr Cys Thr Cys Lys Asn Gly Gly Thr Cys Val Ser Glu Asn Gly Asn
580 585 590

Cys Val Cys Ala Pro Gly Phe Arg Gly Pro Ser Cys Gln Arg Pro Cys
595 600 605

Pro Pro Gly Arg Tyr Gly Lys Arg Cys Val Gln Cys Lys Cys Asn Asn
610 615 620

Asn His Ser Ser Cys His Pro Ser Asp Gly Thr Cys Ser Cys Leu Ala
625 630 635 640

Gly Trp Thr Gly Pro Asp Cys Ser Glu Ala Cys Pro Pro Gly His Trp
645 650 655

Gly Leu Lys Cys Ser Gln Leu Cys Gln Cys His His Gly Gly Thr Cys
660 665 670

His Pro Gln Asp Gly Ser Cys Ile Cys Thr Pro Gly Trp Thr Gly Pro
675 680 685

Asn Cys Leu Glu Gly Cys Pro Pro Arg Met Phe Gly Val Asn Cys Ser
690 695 700

Gln Leu Cys Gln Cys Asp Leu Gly Glu Met Cys His Pro Gln Thr Gly
705 710 715 720

Ala Cys Val Cys Pro Pro Gly His Ser Gly Ala Asp Cys Lys Met Gly
725 730 735

Ser Gln Glu Ser Phe Thr Ile Met Pro Thr Ser Pro Val Thr His Asn
740 745 750

Ser Leu Gly Ala Val Ile Gly Ile Ala Val Leu Gly Thr Leu Val Val
755 760 765

Ala Leu Ile Ala Leu Phe Ile Gly Tyr Arg Gln Trp Gln Lys Gly Lys
770 775 780

Glu His Glu His Leu Ala Val Ala Tyr Ser Thr Gly Arg Leu Asp Gly
785 790 795 800

Ser Asp Tyr Val Met Pro Asp Val Ser Pro Ser Tyr Ser His Tyr Tyr
805 810 815

Ser Asn Pro Ser Tyr His Thr Leu Ser Gln Cys Ser Pro Asn Pro Pro
820 825 830

Pro Pro Asn Lys Val Pro Gly Ser Gln Leu Phe Val Ser Ser Gln Ala
835 840 845

Pro Glu Arg Pro Ser Arg Ala His Gly Arg Glu Asn His Val Thr Leu
850 855 860

Pro Ala Asp Trp Lys His Arg Arg Glu Pro His Glu Arg Gly Ala Ser
865 870 875 880

His Leu Asp Arg Ser Tyr Ser Cys Ser Tyr Ser His Arg Asn Gly Pro
885 890 895

Gly Pro Phe Cys His Lys Gly Pro Ile Ser Glu Glu Gly Leu Gly Ala
900 905 910

Ser Val Met Ser Leu Ser Ser Glu Asn Pro Tyr Ala Thr Ile Arg Asp
915 920 925

Leu Pro Ser Leu Pro Gly Glu Pro Arg Glu Ser Gly Tyr Val Glu Met
930 935 940

Lys Gly Pro Pro Ser Val Ser Pro Pro Arg Gln Ser Leu His Leu Arg
945 950 955 960

Asp Arg Gln Gln Arg Gln Leu Gln Pro Gln Arg Asp Ser Gly Thr Tyr
965 970 975

Glu Gln Pro Ser Pro Leu Ser His Asn Glu Glu Ser Leu Gly Ser Thr
980 985 990

Pro Pro Leu Pro Pro Gly Leu Pro Pro Gly Gln Tyr Asp Ser Pro Lys
995 1000 1005

Asn Ser His Ile Pro Gly His Tyr Asp Leu Pro Pro Val Arg His Pro
1010 1015 1020

Pro Ser Pro Pro Ser Arg Arg Gln Asp Arg
1025 1030

<210> 32

<211> 1034

<212> PRT

<213> Mus musculus

<400> 32

Met Pro Leu Cys Pro Leu Leu Leu Ala Leu Gly Leu Arg Leu Thr
1 5 10 15

Gly Thr Leu Asn Ser Asn Asp Pro Asn Val Cys Thr Phe Trp Glu Ser
20 25 30

Phe Thr Thr Thr Lys Glu Ser His Leu Arg Pro Phe Ser Leu Leu
35 40 45

Pro Ala Glu Ser Cys His Arg Pro Trp Glu Asp Pro His Thr Cys Ala
50 55 60

Gln Pro Thr Val Val Tyr Arg Thr Val Tyr Arg Gln Val Val Lys Met
65 70 75 80

Asp Ser Arg Pro Arg Leu Gln Cys Cys Arg Gly Tyr Tyr Glu Ser Arg
85 90 95

Gly Ala Cys Val Pro Leu Cys Ala Gln Glu Cys Val His Gly Arg Cys

100 105 110

Val Ala Pro Asn Gln Cys Gln Cys Ala Pro Gly Trp Arg Gly Gly Asp
115 120 125

Cys Ser Ser Glu Cys Ala Pro Gly Met Trp Gly Pro Gln Cys Asp Lys
130 135 140

Phe Cys His Cys Gly Asn Asn Ser Ser Cys Asp Pro Lys Ser Gly Thr
145 150 155 160

Cys Phe Cys Pro Ser Gly Leu Gln Pro Pro Asn Cys Leu Gln Pro Cys
165 170 175

Pro Ala Gly His Tyr Gly Pro Ala Cys Gln Phe Asp Cys Gln Cys Tyr
180 185 190

Gly Ala Ser Cys Asp Pro Gln Asp Gly Ala Cys Phe Cys Pro Pro Gly
195 200 205

Arg Ala Gly Pro Ser Cys Asn Val Pro Cys Ser Gln Gly Thr Asp Gly
210 215 220

Phe Phe Cys Pro Arg Thr Tyr Pro Cys Gln Asn Gly Gly Val Pro Gln
225 230 235 240

Gly Ser Gln Gly Ser Cys Ser Cys Pro Pro Gly Trp Met Gly Val Ile
245 250 255

Cys Ser Leu Pro Cys Pro Glu Gly Phe His Gly Pro Asn Cys Thr Gln
260 265 270

Glu Cys Arg Cys His Asn Gly Gly Leu Cys Asp Arg Phe Thr Gly Gln
275 280 285

Cys His Cys Ala Pro Gly Tyr Ile Gly Asp Arg Cys Gln Glu Glu Cys
290 295 300

Pro Val Gly Arg Phe Gly Gln Asp Cys Ala Glu Thr Cys Asp Cys Ala
305 310 315 320

Pro Gly Ala Arg Cys Phe Pro Ala Asn Gly Ala Cys Leu Cys Glu His
325 330 335

Gly Phe Thr Gly Asp Arg Cys Thr Glu Arg Leu Cys Pro Asp Gly Arg
340 345 350

Tyr Gly Leu Ser Cys Gln Glu Pro Cys Thr Cys Asp Pro Glu His Ser

355	360	365
Leu Ser Cys His Pro Met His Gly Glu Cys Ser Cys Gln Pro Gly Trp		
370	375	380
Ala Gly Leu His Cys Asn Glu Ser Cys Pro Gln Asp Thr His Gly Pro		
385	390	395
Gly Cys Gln Glu His Cys Leu Cys Leu His Gly Gly Leu Cys Leu Ala		
405	410	415
Asp Ser Gly Leu Cys Arg Cys Ala Pro Gly Tyr Thr Gly Pro His Cys		
420	425	430
Ala Asn Leu Cys Pro Pro Asp Thr Tyr Gly Ile Asn Cys Ser Ser Arg		
435	440	445
Cys Ser Cys Glu Asn Ala Ile Ala Cys Ser Pro Ile Asp Gly Thr Cys		
450	455	460
Ile Cys Lys Glu Gly Trp Gln Arg Gly Asn Cys Ser Val Pro Cys Pro		
465	470	475
Leu Gly Thr Trp Gly Phe Asn Cys Asn Ala Ser Cys Gln Cys Ala His		
485	490	495
Asp Gly Val Cys Ser Pro Gln Thr Gly Ala Cys Thr Cys Thr Pro Gly		
500	505	510
Trp His Gly Ala His Cys Gln Leu Pro Cys Pro Lys Gly Gln Phe Gly		
515	520	525
Glu Gly Cys Ala Ser Val Cys Asp Cys Asp His Ser Asp Gly Cys Asp		
530	535	540
Pro Val His Gly Gln Cys Arg Cys Gln Ala Gly Trp Met Gly Thr Arg		
545	550	555
Cys His Leu Pro Cys Pro Glu Gly Phe Trp Gly Ala Asn Cys Ser Asn		
565	570	575
Thr Cys Thr Cys Lys Asn Gly Gly Thr Cys Val Ser Glu Asn Gly Asn		
580	585	590
Cys Val Cys Ala Pro Gly Phe Arg Gly Pro Ser Cys Gln Arg Pro Cys		
595	600	605
Pro Pro Gly Arg Tyr Gly Lys Arg Cys Val Gln Cys Lys Cys Asn Asn		

610 615 620
Asn His Ser Ser Cys His Pro Ser Asp Gly Thr Cys Ser Cys Leu Ala
625 630 635 640
Gly Trp Thr Gly Pro Asp Cys Ser Glu Ala Cys Pro Pro Gly His Trp
645 650 655
Gly Leu Lys Cys Ser Gln Leu Cys Gln Cys His His Gly Gly Thr Cys
660 665 670
His Pro Gln Asp Gly Ser Cys Ile Cys Thr Pro Gly Trp Thr Gly Pro
675 680 685
Asn Cys Leu Glu Gly Cys Pro Pro Arg Met Phe Gly Val Asn Cys Ser
690 695 700
Gln Leu Cys Gln Cys Asp Leu Gly Glu Met Cys His Pro Glu Thr Gly
705 710 715 720
Ala Cys Val Cys Pro Pro Gly His Ser Gly Ala Asp Cys Lys Met Gly
725 730 735
Ser Gln Glu Ser Phe Thr Ile Met Pro Thr Ser Pro Val Thr His Asn
740 745 750
Ser Leu Gly Ala Val Ile Gly Ile Ala Val Leu Gly Thr Leu Val Val
755 760 765
Ala Leu Ile Ala Leu Phe Ile Gly Tyr Arg Gln Trp Gln Lys Gly Lys
770 775 780
Glu His Glu His Leu Ala Val Ala Tyr Ser Thr Gly Arg Leu Asp Gly
785 790 795 800
Ser Asp Tyr Val Met Pro Asp Val Ser Pro Ser Tyr Ser His Tyr Tyr
805 810 815
Ser Asn Pro Ser Tyr His Thr Leu Ser Gln Cys Ser Pro Asn Pro Pro
820 825 830
Pro Pro Asn Lys Val Pro Gly Ser Gln Leu Phe Val Ser Ser Gln Ala
835 840 845
Pro Glu Arg Pro Ser Arg Ala His Gly Arg Glu Asn His Val Thr Leu
850 855 860
Pro Ala Asp Trp Lys His Arg Arg Glu Pro His Glu Arg Gly Ala Ser

865	870	875	880
His Leu Asp Arg Ser Tyr Ser Cys Ser Tyr Ser His Arg Asn Gly Pro			
885	890	895	
Gly Pro Phe Cys His Lys Gly Pro Ile Ser Glu Glu Gly Leu Gly Ala			
900	905	910	
Ser Val Met Ser Leu Ser Ser Glu Asn Pro Tyr Ala Thr Ile Arg Asp			
915	920	925	
Leu Pro Ser Leu Pro Gly Glu Pro Arg Glu Ser Gly Tyr Val Glu Met			
930	935	940	
Lys Gly Pro Pro Ser Val Ser Pro Pro Arg Gln Ser Leu His Leu Arg			
945	950	955	960
Asp Arg Gln Gln Arg Gln Leu Gln Pro Gln Arg Asp Ser Gly Thr Tyr			
965	970	975	
Glu Gln Pro Ser Pro Leu Ser His Asn Glu Glu Ser Leu Gly Ser Thr			
980	985	990	
Pro Pro Leu Pro Pro Gly Leu Pro Pro Gly His Tyr Asp Ser Pro Lys			
995	1000	1005	
Asn Ser His Ile Pro Gly His Tyr Asp Leu Pro Pro Val Arg His Pro			
1010	1015	1020	
Pro Ser Pro Pro Ser Arg Arg Gln Asp Arg			
1025	1030		

<210> 33

<211> 1140

<212> PRT

<213> Homo sapiens

<400> 33

Met Val Ile Ser Leu Asn Ser Cys Leu Ser Phe Ile Cys Leu Leu Leu			
1	5	10	15

Cys His Trp Ile Gly Thr Ala Ser Pro Leu Asn Leu Glu Asp Pro Asn			
20	25	30	

Val Cys Ser His Trp Glu Ser Tyr Ser Val Thr Val Gln Glu Ser Tyr			
35	40	45	

Pro	His	Pro	Phe	Asp	Gln	Ile	Tyr	Tyr	Thr	Ser	Cys	Thr	Asp	Ile	Leu
50														60	
Asn	Trp	Phe	Lys	Cys	Thr	Arg	His	Arg	Val	Ser	Tyr	Arg	Thr	Ala	Tyr
65														80	
Arg	His	Gly	Glu	Lys	Thr	Met	Tyr	Arg	Arg	Lys	Ser	Gln	Cys	Cys	Pro
														95	
Gly	Phe	Tyr	Glu	Ser	Gly	Glu	Met	Cys	Val	Pro	His	Cys	Ala	Asp	Lys
														100	
Cys	Val	His	Gly	Arg	Cys	Ile	Ala	Pro	Asn	Thr	Cys	Gln	Cys	Glu	Pro
														110	
Gly	Trp	Gly	Gly	Thr	Asn	Cys	Ser	Ser	Ala	Cys	Asp	Gly	Asp	His	Trp
														130	
Gly	Pro	His	Cys	Thr	Ser	Arg	Cys	Gln	Cys	Lys	Asn	Gly	Ala	Leu	Cys
														145	
Asn	Pro	Ile	Thr	Gly	Ala	Cys	His	Cys	Ala	Ala	Gly	Phe	Arg	Gly	Trp
														160	
														175	
Arg	Cys	Glu	Asp	Arg	Cys	Glu	Gln	Gly	Thr	Tyr	Gly	Asn	Asp	Cys	His
														180	
Gln	Arg	Cys	Gln	Cys	Gln	Asn	Gly	Ala	Thr	Cys	Asp	His	Val	Thr	Gly
														195	
Glu	Cys	Arg	Cys	Pro	Pro	Gly	Tyr	Thr	Gly	Ala	Phe	Cys	Glu	Asp	Leu
														210	
Cys	Pro	Pro	Gly	Lys	His	Gly	Pro	Gln	Cys	Glu	Gln	Arg	Cys	Pro	Cys
														225	
Gln	Asn	Gly	Gly	Val	Cys	His	His	Val	Thr	Gly	Glu	Cys	Ser	Cys	Pro
														240	
														245	
Ser	Gly	Trp	Met	Gly	Thr	Val	Cys	Gly	Gln	Pro	Cys	Pro	Glu	Gly	Arg
														260	
Phe	Gly	Lys	Asn	Cys	Ser	Gln	Glu	Cys	Gln	Cys	His	Asn	Gly	Gly	Thr
														275	
Cys	Asp	Ala	Ala	Thr	Gly	Gln	Cys	His	Cys	Ser	Pro	Gly	Tyr	Thr	Gly
														290	
														295	
														300	

Glu	Arg	Cys	Gln	Asp	Glu	Cys	Pro	Val	Gly	Thr	Tyr	Gly	Val	Leu	Cys
305					310					315					320
Ala	Glu	Thr	Cys	Gln	Cys	Val	Asn	Gly	Gly	Lys	Cys	Tyr	His	Val	Ser
					325				330					335	
Gly	Ala	Cys	Leu	Cys	Glu	Ala	Gly	Phe	Ala	Gly	Glu	Arg	Cys	Glu	Ala
					340				345					350	
Arg	Leu	Cys	Pro	Glu	Gly	Leu	Tyr	Gly	Ile	Lys	Cys	Asp	Lys	Arg	Cys
					355				360					365	
Pro	Cys	His	Leu	Glu	Asn	Thr	His	Ser	Cys	His	Pro	Met	Ser	Gly	Glu
					370				375					380	
Cys	Ala	Cys	Lys	Pro	Gly	Trp	Ser	Gly	Leu	Tyr	Cys	Asn	Glu	Thr	Cys
					385				390					400	
Ser	Pro	Gly	Phe	Tyr	Gly	Glu	Ala	Cys	Gln	Gln	Ile	Cys	Ser	Cys	Gln
					405				410					415	
Asn	Gly	Ala	Asp	Cys	Asp	Ser	Val	Thr	Gly	Lys	Cys	Thr	Cys	Ala	Pro
					420				425					430	
Gly	Phe	Lys	Gly	Ile	Asp	Cys	Ser	Thr	Pro	Cys	Pro	Leu	Gly	Thr	Tyr
					435				440					445	
Gly	Ile	Asn	Cys	Ser	Ser	Arg	Cys	Gly	Cys	Lys	Asn	Asp	Ala	Val	Cys
					450				455					460	
Ser	Pro	Val	Asp	Gly	Ser	Cys	Thr	Cys	Lys	Ala	Gly	Trp	His	Gly	Val
					465				470					480	
Asp	Cys	Ser	Ile	Arg	Cys	Pro	Ser	Gly	Thr	Trp	Gly	Phe	Gly	Cys	Asn
					485				490					495	
Leu	Thr	Cys	Gln	Cys	Leu	Asn	Gly	Gly	Ala	Cys	Asn	Thr	Leu	Asp	Gly
					500				505					510	
Thr	Cys	Thr	Cys	Ala	Pro	Gly	Trp	Arg	Gly	Glu	Lys	Cys	Glu	Leu	Pro
					515				520					525	
Cys	Gln	Asp	Gly	Thr	Tyr	Gly	Leu	Asn	Cys	Ala	Glu	Arg	Cys	Asp	Cys
					530				535					540	
Ser	His	Ala	Asp	Gly	Cys	His	Pro	Thr	Thr	Gly	His	Cys	Arg	Cys	Leu
					545				550					560	

Pro Gly Trp Ser Gly Val His Cys Asp Ser Val Cys Ala Glu Gly Arg
 565 570 575

 Trp Gly Pro Asn Cys Ser Leu Pro Cys Tyr Cys Lys Asn Gly Ala Ser
 580 585 590

 Cys Ser Pro Asp Asp Gly Ile Cys Glu Cys Ala Pro Gly Phe Arg Gly
 595 600 605

 Thr Thr Cys Gln Arg Ile Cys Ser Pro Gly Phe Tyr Gly His Arg Cys
 610 615 620

 Ser Gln Thr Cys Pro Gln Cys Val His Ser Ser Gly Pro Cys His His
 625 630 635 640

 Ile Thr Gly Leu Cys Asp Cys Leu Pro Gly Phe Thr Gly Ala Leu Cys
 645 650 655

 Asn Glu Val Cys Pro Ser Gly Arg Phe Gly Lys Asn Cys Ala Gly Ile
 660 665 670

 Cys Thr Cys Thr Asn Asn Gly Thr Cys Asn Pro Ile Asp Arg Ser Cys
 675 680 685

 Gln Cys Tyr Pro Gly Trp Ile Gly Ser Asp Cys Ser Gln Pro Cys Pro
 690 695 700

 Pro Ala His Trp Gly Pro Asn Cys Ile His Thr Cys Asn Cys His Asn
 705 710 715 720

 Gly Ala Phe Cys Ser Ala Tyr Asp Gly Glu Cys Lys Cys Thr Pro Gly
 725 730 735

 Trp Thr Gly Leu Tyr Cys Thr Gln Arg Cys Pro Leu Gly Phe Tyr Gly
 740 745 750

 Lys Asp Cys Ala Leu Ile Cys Gln Cys Gln Asn Gly Ala Asp Cys Asp
 755 760 765

 His Ile Ser Gly Gln Cys Thr Cys Arg Thr Gly Phe Met Gly Arg His
 770 775 780

 Cys Glu Gln Lys Cys Pro Ser Gly Thr Tyr Gly Tyr Cys Arg Gln
 785 790 795 800

 Ile Cys Asp Cys Leu Asn Asn Ser Thr Cys Asp His Ile Thr Gly Thr
 805 810 815

Cys	Tyr	Cys	Ser	Pro	Gly	Trp	Lys	Gly	Ala	Arg	Cys	Asp	Gln	Ala	Gly
820															
Val	Ile	Ile	Val	Gly	Asn	Leu	Asn	Ser	Leu	Ser	Arg	Thr	Ser	Thr	Ala
835															
Leu	Pro	Ala	Asp	Ser	Tyr	Gln	Ile	Gly	Ala	Ile	Ala	Gly	Ile	Ile	Ile
850															
Leu	Val	Leu	Val	Val	Leu	Phe	Leu	Leu	Ala	Leu	Phe	Ile	Ile	Tyr	Arg
865															
His	Lys	Gln	Lys	Gly	Lys	Glu	Ser	Ser	Met	Pro	Ala	Val	Thr	Tyr	Thr
885															
Pro	Ala	Met	Arg	Val	Val	Asn	Ala	Asp	Tyr	Thr	Ile	Ser	Gly	Thr	Leu
900															
Pro	His	Ser	Asn	Gly	Gly	Asn	Ala	Asn	Ser	His	Tyr	Phe	Thr	Asn	Pro
915															
Ser	Tyr	His	Thr	Leu	Thr	Gln	Cys	Ala	Thr	Ser	Pro	His	Val	Asn	Asn
930															
Arg	Asp	Arg	Met	Thr	Val	Thr	Lys	Ser	Lys	Asn	Asn	Gln	Leu	Phe	Val
945															
Asn	Leu	Lys	Asn	Val	Asn	Pro	Gly	Lys	Arg	Gly	Pro	Val	Gly	Asp	Cys
965															
Thr	Gly	Thr	Leu	Pro	Ala	Asp	Trp	Lys	His	Gly	Gly	Tyr	Leu	Asn	Glu
980															
Leu	Gly	Ala	Phe	Gly	Leu	Asp	Arg	Ser	Tyr	Met	Gly	Lys	Ser	Leu	Lys
995															
Asp	Leu	Gly	Lys	Asn	Ser	Glu	Tyr	Asn	Ser	Ser	Asn	Cys	Ser	Leu	Ser
1010															
Ser	Ser	Glu	Asn	Pro	Tyr	Ala	Thr	Ile	Lys	Asp	Pro	Pro	Val	Leu	Ile
1025															
Pro	Lys	Ser	Ser	Glu	Cys	Gly	Tyr	Val	Glu	Met	Lys	Ser	Pro	Ala	Arg
1045															
Arg	Asp	Ser	Pro	Tyr	Ala	Glu	Ile	Asn	Asn	Ser	Thr	Ser	Ala	Asn	Arg
1060															

Asn Val Tyr Glu Val Glu Pro Thr Val Ser Val Val Gln Gly Val Phe
1075 1080 1085

Ser Asn Asn Gly Arg Leu Ser Gln Asp Pro Tyr Asp Leu Pro Lys Asn
1090 1095 1100

Ser His Ile Pro Cys His Tyr Asp Leu Leu Pro Val Arg Asp Ser Ser
1105 1110 1115 1120

Ser Ser Pro Lys Gln Glu Asp Ser Gly Gly Ser Ser Ser Asn Ser Ser
1125 1130 1135

Ser Ser Ser Glu
1140

<210> 34

<211> 969

<212> PRT

<213> Homo sapiens

<400> 34

Met His Thr Pro Ser Ile Arg Ser Ile Thr His Asp Ala Gln Thr Ser
1 5 10 15

Ser Thr Gly Ser Ser Ala Pro Gly Thr Ala Leu Cys Thr Glu Glu Cys
20 25 30

Val His Gly Arg Cys Val Ser Pro Asp Thr Cys His Cys Glu Pro Gly
35 40 45

Trp Gly Gly Pro Asp Cys Ser Ser Gly Cys Asp Ser Asp His Trp Gly
50 55 60

Pro His Cys Ser Asn Arg Cys Gln Cys Gln Asn Gly Ala Leu Cys Asn
65 70 75 80

Pro Ile Thr Gly Ala Cys Val Cys Ala Ala Gly Phe Arg Gly Trp Arg
85 90 95

Cys Glu Glu Leu Cys Ala Pro Gly Thr His Gly Lys Gly Cys Gln Leu
100 105 110

Pro Cys Gln Cys Arg His Gly Ala Ser Cys Asp Pro Arg Ala Gly Glu
115 120 125

Cys Leu Cys Ala Pro Gly Tyr Thr Gly Val Tyr Cys Glu Glu Leu Cys
130 135 140

Pro Pro Gly Ser His Gly Ala His Cys Glu Leu Arg Cys Pro Cys Gln
145 150 155 160

Asn Gly Gly Thr Cys His His Ile Thr Gly Glu Cys Ala Cys Pro Pro
165 170 175

Gly Trp Thr Gly Ala Val Cys Ala Gln Pro Cys Pro Pro Gly Thr Phe
180 185 190

Gly Gln Asn Cys Ser Gln Asp Cys Pro Cys His His Gly Gly Gln Cys
195 200 205

Asp His Val Thr Gly Gln Cys His Cys Thr Ala Gly Tyr Met Gly Asp
210 215 220

Arg Cys Gln Glu Glu Cys Pro Phe Gly Ser Phe Gly Phe Gln Cys Ser
225 230 235 240

Gln Arg Cys Asp Cys His Asn Gly Gly Gln Cys Ser Pro Thr Thr Gly
245 250 255

Ala Cys Glu Cys Glu Pro Gly Tyr Lys Gly Pro Arg Cys Gln Glu Arg
260 265 270

Leu Cys Pro Glu Gly Leu His Gly Pro Gly Cys Thr Leu Pro Cys Pro
275 280 285

Cys Asp Ala Asp Asn Thr Ile Ser Cys His Pro Val Thr Gly Ala Cys
290 295 300

Thr Cys Gln Pro Gly Trp Ser Gly His His Cys Asn Glu Ser Cys Pro
305 310 315 320

Val Gly Tyr Tyr Gly Asp Gly Cys Gln Leu Pro Cys Thr Cys Gln Asn
325 330 335

Gly Ala Asp Cys His Ser Ile Thr Gly Gly Cys Thr Cys Ala Pro Gly
340 345 350

Phe Met Gly Glu Val Cys Ala Val Ser Cys Ala Ala Gly Thr Tyr Gly
355 360 365

Pro Asn Cys Ser Ser Ile Cys Ser Cys Asn Asn Gly Gly Thr Cys Ser
370 375 380

Pro Val Asp Gly Ser Cys Thr Cys Lys Glu Gly Trp Gln Gly Leu Asp
385 390 395 400

Cys Thr Leu Pro Cys Pro Ser Gly Thr Trp Gly Leu Asn Cys Asn Glu
 405 410 415

 Ser Cys Thr Cys Ala Asn Gly Ala Ala Cys Ser Pro Ile Asp Gly Ser
 420 425 430

 Cys Ser Cys Thr Pro Gly Trp Leu Gly Asp Thr Cys Glu Leu Pro Cys
 435 440 445

 Pro Asp Gly Thr Phe Gly Leu Asn Cys Ser Glu His Cys Asp Cys Ser
 450 455 460

 His Ala Asp Gly Cys Asp Pro Val Thr Gly His Cys Cys Cys Leu Ala
 465 470 475 480

 Gly Trp Thr Gly Ile Arg Cys Asp Ser Thr Cys Pro Pro Gly Arg Trp
 485 490 495

 Gly Pro Asn Cys Ser Val Ser Cys Ser Cys Glu Asn Gly Gly Ser Cys
 500 505 510

 Ser Pro Glu Asp Gly Ser Cys Glu Cys Ala Pro Gly Phe Arg Gly Pro
 515 520 525

 Leu Cys Gln Arg Ile Cys Pro Pro Gly Phe Tyr Gly His Gly Cys Ala
 530 535 540

 Gln Pro Cys Pro Leu Cys Val His Ser Ser Arg Pro Cys His His Ile
 545 550 555 560

 Ser Gly Ile Cys Glu Cys Leu Pro Gly Phe Ser Gly Ala Leu Cys Asn
 565 570 575

 Gln Val Cys Ala Gly Gly Tyr Phe Gly Gln Asp Cys Ala Gln Leu Cys
 580 585 590

 Ser Cys Ala Asn Asn Gly Thr Cys Ser Pro Ile Asp Gly Ser Cys Gln
 595 600 605

 Cys Phe Pro Gly Trp Ile Gly Lys Asp Cys Ser Gln Ala Cys Pro Pro
 610 615 620

 Gly Phe Trp Gly Pro Ala Cys Phe His Ala Cys Ser Cys His Asn Gly
 625 630 635 640

 Ala Ser Cys Ser Ala Glu Asp Gly Ala Cys His Cys Thr Pro Gly Trp
 645 650 655

Thr Gly Leu Phe Cys Thr Gln Arg Cys Pro Ala Ala Phe Phe Gly Lys
660 665 670

Asp Cys Gly Arg Val Cys Gln Cys Gln Asn Gly Ala Ser Cys Asp His
675 680 685

Ile Ser Gly Lys Cys Thr Cys Arg Thr Gly Phe Thr Gly Gln His Cys
690 695 700

Glu Gln Arg Cys Ala Pro Gly Thr Phe Gly Tyr Gly Cys Gln Gln Leu
705 710 715 720

Cys Glu Cys Met Asn Asn Ser Thr Cys Asp His Val Thr Gly Thr Cys
725 730 735

Tyr Cys Ser Pro Gly Phe Lys Gly Ile Arg Cys Asp Gln Ala Ala Leu
740 745 750

Met Met Glu Glu Leu Asn Pro Tyr Thr Lys Ile Ser Pro Ala Leu Gly
755 760 765

Ala Glu Arg His Ser Val Gly Ala Val Thr Gly Ile Met Leu Leu Leu
770 775 780

Phe Phe Ile Val Val Leu Leu Gly Leu Phe Ala Trp His Arg Arg Arg
785 790 795 800

Gln Lys Glu Lys Gly Arg Asp Leu Ala Pro Arg Val Ser Tyr Thr Pro
805 810 815

Ala Met Arg Met Thr Ser Thr Asp Tyr Ser Leu Ser Gly Ala Cys Gly
820 825 830

Met Asp Arg Arg Gln Asn Thr Tyr Ile Met Asp Lys Gly Phe Lys Asp
835 840 845

Tyr Met Lys Glu Ser Val Cys Ser Ser Ser Thr Cys Ser Leu Asn Ser
850 855 860

Ser Glu Asn Pro Tyr Ala Thr Ile Lys Asp Pro Pro Ile Leu Thr Cys
865 870 875 880

Lys Leu Pro Glu Ser Ser Tyr Val Glu Met Lys Ser Pro Val His Met
885 890 895

Gly Ser Pro Tyr Thr Asp Val Pro Ser Leu Ser Thr Ser Asn Lys Asn
900 905 910

Ile Tyr Glu Val Glu Pro Thr Val Ser Val Val Gln Glu Gly Cys Gly
915 920 925

His Asn Ser Ser Tyr Ile Gln Asn Ala Tyr Asp Leu Pro Arg Asn Ser
930 935 940

His Ile Pro Gly His Tyr Asp Leu Leu Pro Val Arg Gln Ser Pro Ala
945 950 955 960

Asn Gly Pro Ser Gln Asp Lys Gln Ser
965

<210> 35

<211> 969

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (848)..(889)

<223> Where Xaa is any amino acid

<400> 35

Met His Thr Pro Ser Ile Arg Ser Ile Thr His Asp Ala Gln Thr Ser
1 5 10 15

Ser Thr Gly Ser Ser Ala Pro Gly Thr Ala Leu Cys Thr Glu Glu Cys
20 25 30

Val His Gly Arg Cys Val Ser Pro Asp Thr Cys His Cys Glu Pro Gly
35 40 45

Trp Gly Gly Pro Asp Cys Ser Ser Gly Cys Asp Ser Asp His Trp Gly
50 55 60

Pro His Cys Ser Asn Arg Cys Gln Cys Gln Asn Gly Ala Leu Cys Asn
65 70 75 80

Pro Ile Thr Gly Ala Cys Val Cys Ala Ala Gly Phe Arg Gly Trp Arg
85 90 95

Cys Glu Glu Leu Cys Ala Pro Gly Thr His Gly Lys Gly Cys Gln Leu
100 105 110

Pro Cys Gln Cys Arg His Gly Ala Ser Cys Asp Pro Arg Ala Gly Glu
115 120 125

Cys Leu Cys Ala Pro Gly Tyr Thr Gly Val Tyr Cys Glu Glu Leu Cys
130 135 140

Pro Pro Gly Ser His Gly Ala His Cys Glu Leu Arg Cys Pro Cys Gln
145 150 155 160

Asn Gly Gly Thr Cys His His Ile Thr Gly Glu Cys Ala Cys Pro Pro
165 170 175

Gly Trp Thr Gly Ala Val Cys Ala Gln Pro Cys Pro Pro Gly Thr Phe
180 185 190

Gly Gln Asn Cys Ser Gln Asp Cys Pro Cys His His Gly Gly Gln Cys
195 200 205

Asp His Val Thr Gly Gln Cys His Cys Thr Ala Gly Tyr Met Gly Asp
210 215 220

Arg Cys Gln Glu Glu Cys Pro Phe Gly Ser Phe Gly Phe Gln Cys Ser
225 230 235 240

Gln His Cys Asp Cys His Asn Gly Gly Gln Cys Ser Pro Thr Thr Gly
245 250 255

Ala Cys Glu Cys Glu Pro Gly Tyr Lys Gly Pro Arg Cys Gln Glu Arg
260 265 270

Leu Cys Pro Glu Gly Leu His Gly Pro Gly Cys Thr Leu Pro Cys Pro
275 280 285

Cys Asp Ala Asp Asn Thr Ile Ser Cys His Pro Val Thr Gly Ala Cys
290 295 300

Thr Cys Gln Pro Gly Trp Ser Gly His His Cys Asn Glu Ser Cys Pro
305 310 315 320

Val Gly Tyr Tyr Gly Asp Gly Cys Gln Leu Pro Cys Thr Cys Gln Asn
325 330 335

Gly Ala Asp Cys His Ser Ile Thr Gly Gly Cys Thr Cys Ala Pro Gly
340 345 350

Phe Met Gly Glu Val Cys Ala Val Ser Cys Ala Ala Gly Thr Tyr Gly
355 360 365

Pro Asn Cys Ser Ser Ile Cys Ser Cys Asn Asn Gly Gly Thr Cys Ser
370 375 380

Pro Val Asp Gly Ser Cys Thr Cys Lys Glu Gly Trp Gln Gly Leu Asp
 385 390 395 400

 Cys Thr Leu Pro Cys Pro Ser Gly Thr Trp Gly Leu Asn Cys Asn Glu
 405 410 415

 Ser Cys Thr Cys Ala Asn Gly Ala Ala Cys Ser Pro Ile Asp Gly Ser
 420 425 430

 Cys Ser Cys Thr Pro Gly Trp Leu Gly Asp Thr Cys Glu Leu Pro Cys
 435 440 445

 Pro Asp Gly Thr Phe Gly Leu Asn Cys Ser Glu His Cys Asp Cys Ser
 450 455 460

 His Ala Asp Gly Cys Asp Pro Val Thr Gly His Cys Cys Cys Leu Ala
 465 470 475 480

 Gly Trp Thr Gly Ile Arg Cys Asp Ser Thr Cys Pro Pro Gly Arg Trp
 485 490 495

 Gly Pro Asn Cys Ser Val Ser Cys Ser Cys Glu Asn Gly Gly Ser Cys
 500 505 510

 Ser Pro Glu Asp Gly Ser Cys Glu Cys Ala Pro Gly Phe Arg Gly Pro
 515 520 525

 Leu Cys Gln Arg Ile Cys Pro Pro Gly Phe Tyr Gly His Gly Cys Ala
 530 535 540

 Gln Pro Cys Pro Leu Cys Val His Ser Ser Arg Pro Cys His His Ile
 545 550 555 560

 Ser Gly Ile Cys Glu Cys Leu Pro Gly Phe Ser Gly Ala Leu Cys Asn
 565 570 575

 Gln Val Cys Ala Gly Gly Tyr Phe Gly Gln Asp Cys Ala Gln Leu Cys
 580 585 590

 Ser Cys Ala Asn Asn Gly Thr Cys Ser Pro Ile Asp Gly Ser Cys Gln
 595 600 605

 Cys Phe Pro Gly Trp Ile Gly Lys Asp Cys Ser Gln Ala Cys Pro Pro
 610 615 620

 Gly Phe Trp Gly Pro Ala Cys Phe His Ala Cys Ser Cys His Asn Gly
 625 630 635 640

Ala Ser Cys Ser Ala Glu Asp Gly Ala Cys His Cys Thr Pro Gly Trp			
645	650	655	
Thr Gly Leu Phe Cys Thr Gln Arg Cys Pro Ala Ala Phe Phe Gly Lys			
660	665	670	
Asp Cys Gly Arg Val Cys Gln Cys Gln Asn Gly Ala Ser Cys Asp His			
675	680	685	
Ile Ser Gly Lys Cys Thr Cys Arg Thr Gly Phe Thr Gly Gln His Cys			
690	695	700	
Glu Gln Arg Cys Ala Pro Gly Thr Phe Gly Tyr Gly Cys Gln Gln Leu			
705	710	715	720
Cys Glu Cys Met Asn Asn Ser Thr Cys Asp His Val Thr Gly Thr Cys			
725	730	735	
Tyr Cys Ser Pro Gly Phe Lys Gly Ile Arg Cys Asp Gln Ala Ala Leu			
740	745	750	
Met Met Glu Glu Leu Asn Pro Tyr Thr Lys Ile Ser Pro Ala Leu Gly			
755	760	765	
Ala Glu Arg His Ser Val Gly Ala Val Thr Gly Ile Met Leu Leu Leu			
770	775	780	
Phe Leu Ile Val Val Leu Leu Gly Leu Phe Ala Trp His Arg Arg Arg			
785	790	795	800
Gln Lys Glu Lys Gly Arg Asp Leu Ala Pro Arg Val Ser Tyr Thr Pro			
805	810	815	
Ala Met Arg Met Thr Ser Thr Asp Tyr Ser Leu Ser Gly Ala Cys Gly			
820	825	830	
Met Asp Arg Arg Gln Asn Thr Tyr Ile Met Asp Lys Gly Phe Lys Xaa			
835	840	845	
Xaa			
850	855	860	
Xaa			
865	870	875	880
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Met Lys Ser Pro Val His Met			
885	890	895	

Gly Ser Pro Tyr Thr Asp Val Pro Ser Leu Ser Thr Ser Asn Lys Asn
900 905 910

Ile Tyr Glu Val Glu Pro Thr Val Ser Val Val Gln Glu Gly Cys Gly
915 920 925

His Asn Ser Ser Tyr Ile Gln Asn Ala Tyr Asp Leu Pro Arg Asn Ser
930 935 940

His Ile Pro Gly His Tyr Asp Leu Leu Pro Val Arg Gln Ser Pro Ala
945 950 955 960

Asn Gly Pro Ser Gln Asp Lys Gln Ser
965

<210> 36

<211> 1234

<212> PRT

<213> Homo sapiens

<400> 36

Met Leu Ala Ser Pro Ala Thr Glu Thr Thr Val Leu Met Ser Gln Thr
1 5 10 15

Glu Ala Asp Leu Ala Leu Arg Pro Pro Pro Pro Leu Gly Thr Ala Gly
20 25 30

Gln Pro Arg Leu Gly Pro Pro Pro Arg Arg Ala Arg Arg Phe Ser Gly
35 40 45

Lys Ala Glu Pro Arg Pro Arg Ser Ser Arg Leu Ser Arg Arg Ser Ser
50 55 60

Val Asp Leu Gly Leu Leu Ser Ser Trp Ser Leu Pro Ala Ser Pro Ala
65 70 75 80

Pro Asp Pro Pro Asp Pro Pro Asp Ser Ala Gly Pro Gly Pro Ala Arg
85 90 95

Ser Pro Pro Ser Ser Lys Glu Pro Pro Glu Gly Thr Trp Thr Glu Gly
100 105 110

Ala Pro Val Lys Ala Ala Glu Asp Ser Ala Arg Pro Glu Leu Pro Asp
115 120 125

Ser Ala Val Gly Pro Gly Ser Arg Glu Pro Leu Arg Val Pro Glu Ala

130	135	140
Val Ala Leu Glu Arg Arg Arg Glu Gln Glu Glu Lys Glu Asp Met Glu		
145	150	155
Thr Gln Ala Val Ala Thr Ser Pro Asp Gly Arg Tyr Leu Lys Phe Asp		
165	170	175
Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val Arg Gly Leu Asp Thr		
180	185	190
Asp Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Thr Arg Lys Leu		
195	200	205
Ser Arg Ala Glu Arg Gln Arg Phe Ser Glu Glu Val Glu Met Leu Lys		
210	215	220
Gly Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Lys Ser		
225	230	235
Val Leu Arg Gly Gln Val Cys Ile Val Leu Val Thr Glu Leu Met Thr		
245	250	255
Ser Gly Thr Leu Lys Thr Leu Arg Arg Phe Arg Glu Met Lys Pro Arg		
260	265	270
Val Leu Gln Arg Trp Ser Arg Gln Ile Leu Arg Gly Leu His Phe Leu		
275	280	285
His Ser Arg Val Pro Pro Ile Leu His Arg Asp Leu Lys Cys Asp Asn		
290	295	300
Val Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp Leu Gly		
305	310	315
Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile Gly Thr		
325	330	335
Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp Glu Ala		
340	345	350
Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala Thr Ser		
355	360	365
Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Lys Val Thr		
370	375	380
Ser Gly Arg Lys Pro Asn Ser Phe His Lys Val Lys Ile Pro Glu Val		

385 390 395 400
Lys Glu Ile Ile Glu Gly Cys Ile Arg Thr Asp Lys Asn Glu Arg Phe
405 410 415
Thr Ile Gln Asp Leu Leu Ala His Ala Phe Phe Arg Glu Glu Arg Gly
420 425 430
Val His Val Glu Leu Ala Glu Glu Asp Asp Gly Glu Lys Pro Gly Leu
435 440 445
Lys Leu Trp Leu Arg Met Glu Asp Ala Arg Arg Gly Gly Arg Pro Arg
450 455 460
Asp Asn Gln Ala Ile Glu Phe Leu Phe Gln Leu Gly Arg Ala Ala Glu
465 470 475 480
Glu Val Ala Gln Glu Met Val Ala Leu Gly Leu Val Cys Glu Ala Asp
485 490 495
Tyr Gln Pro Val Ala Arg Ala Val Arg Glu Arg Val Ala Ala Ile Gln
500 505 510
Arg Lys Arg Lys Leu Arg Lys Ala Arg Glu Leu Glu Ala Leu Pro Pro
515 520 525
Glu Pro Gly Pro Pro Pro Ala Thr Val Pro Met Ala Pro Gly Pro Pro
530 535 540
Ser Val Phe Pro Pro Glu Pro Glu Glu Pro Glu Ala Asp Gln His Gln
545 550 555 560
Pro Phe Leu Phe Arg His Ala Ser Tyr Ser Ser Thr Thr Ser Asp Cys
565 570 575
Glu Thr Asp Gly Tyr Leu Ser Ser Ser Gly Phe Leu Asp Ala Ser Asp
580 585 590
Pro Ala Leu Gln Pro Pro Gly Gly Val Pro Ser Ser Leu Ala Glu Ser
595 600 605
His Leu Cys Leu Pro Ser Ala Phe Ala Leu Ser Ile Pro Arg Ser Gly
610 615 620
Pro Gly Ser Asp Phe Ser Pro Gly Asp Ser Tyr Ala Ser Asp Ala Ala
625 630 635 640
Ser Gly Leu Ser Asp Val Gly Glu Gly Met Gly Gln Met Arg Arg Pro

645	650	655
Pro Gly Arg Asn Leu Arg Arg Arg Pro Arg Ser Arg Leu Arg Val Thr		
660	665	670
Ser Val Ser Asp Gln Asn Asp Arg Val Val Glu Cys Gln Leu Gln Thr		
675	680	685
His Asn Ser Lys Met Val Thr Phe Arg Phe Asp Leu Asp Gly Asp Ser		
690	695	700
Pro Glu Glu Ile Ala Ala Met Val Tyr Asn Glu Phe Ile Leu Pro		
705	710	715
720		
Ser Glu Arg Asp Gly Phe Leu Arg Arg Ile Arg Glu Ile Ile Gln Arg		
725	730	735
Val Glu Thr Leu Leu Lys Arg Asp Thr Gly Pro Met Glu Ala Ala Glu		
740	745	750
Asp Thr Leu Ser Pro Gln Glu Glu Pro Ala Pro Leu Pro Ala Leu Pro		
755	760	765
Val Pro Leu Pro Asp Pro Ser Asn Glu Glu Leu Gln Ser Ser Thr Ser		
770	775	780
Leu Glu His Arg Ser Trp Thr Ala Phe Ser Thr Ser Ser Ser Pro		
785	790	795
800		
Gly Thr Pro Leu Ser Pro Gly Asn Pro Phe Ser Pro Gly Thr Pro Ile		
805	810	815
Ser Pro Gly Pro Ile Phe Pro Ile Thr Ser Pro Pro Cys His Pro Ser		
820	825	830
Pro Ser Pro Phe Ser Pro Ile Ser Ser Gln Val Ser Ser Asn Pro Ser		
835	840	845
Pro His Pro Thr Ser Ser Pro Leu Pro Phe Ser Ser Ser Thr Pro Glu		
850	855	860
Phe Pro Val Pro Leu Ser Gln Cys Pro Trp Ser Ser Leu Pro Thr Thr		
865	870	875
880		
Ser Pro Pro Thr Phe Ser Pro Thr Cys Ser Gln Val Thr Leu Ser Ser		
885	890	895
Pro Phe Phe Pro Pro Cys Pro Ser Thr Ser Ser Phe Pro Ser Thr Thr		

900 905 910
Ala Ala Pro Leu Leu Ser Leu Ala Ser Ala Phe Ser Leu Ala Val Met
915 920 925
Thr Val Ala Gln Ser Leu Ser Pro Ser Pro Gly Leu Leu Ser Gln Ser
930 935 940
Pro Pro Ala Pro Pro Ser Pro Leu Pro Ser Leu Pro Leu Pro Pro Pro
945 950 955 960
Val Ala Pro Gly Gly Gln Glu Ser Pro Ser Pro His Thr Ala Glu Val
965 970 975
Glu Ser Glu Ala Ser Pro Pro Ala Arg Pro Leu Pro Gly Glu Ala
980 985 990
Arg Leu Ala Pro Ile Ser Glu Glu Gly Lys Pro Gln Leu Val Gly Arg
995 1000 1005
Phe Gln Val Thr Ser Ser Lys Glu Pro Ala Glu Pro Leu Pro Leu Gln
1010 1015 1020
Pro Thr Ser Pro Thr Leu Ser Gly Ser Pro Lys Pro Ser Thr Pro Gln
1025 1030 1035 1040
Leu Thr Ser Glu Ser Ser Asp Thr Glu Asp Ser Ala Gly Gly Pro
1045 1050 1055
Glu Thr Arg Glu Ala Leu Ala Glu Ser Asp Arg Ala Ala Glu Gly Leu
1060 1065 1070
Gly Ala Gly Val Glu Glu Glu Gly Asp Asp Gly Lys Glu Pro Gln Val
1075 1080 1085
Gly Gly Ser Pro Gln Pro Leu Ser His Pro Ser Pro Val Trp Met Asn
1090 1095 1100
Tyr Ser Tyr Ser Ser Leu Cys Leu Ser Ser Glu Glu Ser Glu Ser Ser
1105 1110 1115 1120
Gly Glu Glu Glu Phe Trp Ala Glu Leu Gln Ser Leu Arg Gln Lys His
1125 1130 1135
Leu Ser Glu Val Glu Thr Leu Gln Thr Leu Gln Lys Lys Glu Ile Glu
1140 1145 1150
Asp Leu Tyr Ser Arg Leu Gly Lys Gln Pro Pro Pro Gly Ile Val Ala

1155	1160	1165
Pro Ala Ala Met Leu Ser Ser Arg Gln Arg Arg Leu Ser Lys Gly Ser		
1170	1175	1180
Phe Pro Thr Ser Arg Arg Asn Ser Leu Gln Arg Ser Glu Pro Pro Gly		
1185	1190	1195
Pro Gly Ile Met Arg Arg Asn Ser Leu Ser Gly Ser Ser Thr Gly Ser		
1205	1210	1215
Gln Glu Gln Arg Ala Ser Lys Gly Val Thr Phe Ala Gly Asp Val Gly		
1220	1225	1230
Arg Met		

<210> 37		
<211> 1231		
<212> PRT		
<213> Homo sapiens		
<400> 37		
Met Ser Gln Thr Glu Ala Asp Leu Ala Leu Arg Pro Pro Pro Pro Leu		
1	5	10
		15
Gly Thr Ala Gly Gln Pro Arg Leu Gly Pro Pro Pro Arg Arg Ala Arg		
20	25	30
Arg Phe Ser Gly Lys Ala Glu Pro Arg Pro Arg Ser Ser Arg Leu Ser		
35	40	45
Arg Arg Ser Ser Val Asp Leu Gly Leu Leu Ser Ser Trp Ser Leu Pro		
50	55	60
Ala Ser Pro Ala Pro Asp Pro Pro Asp Pro Pro Asp Ser Ala Gly Pro		
65	70	75
		80
Gly Pro Ala Arg Ser Pro Pro Pro Ser Ser Lys Glu Pro Pro Glu Gly		
85	90	95
Thr Trp Thr Glu Gly Ala Pro Val Lys Ala Ala Glu Asp Ser Ala Arg		
100	105	110
Pro Glu Leu Pro Asp Ser Ala Val Gly Pro Gly Ser Arg Glu Pro Leu		
115	120	125

Arg Val Pro Glu Ala Val Ala Leu Glu Arg Arg Arg Glu Gln Glu Glu
 130 135 140

Lys Glu Asp Met Glu Thr Gln Ala Val Ala Thr Ser Pro Asp Gly Arg
 145 150 155 160

Tyr Leu Lys Phe Asp Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val
 165 170 175

Tyr Arg Gly Leu Asp Thr Asp Thr Thr Val Glu Val Ala Trp Cys Glu
 180 185 190

Leu Gln Thr Arg Lys Leu Ser Arg Ala Glu Arg Gln Arg Phe Ser Glu
 195 200 205

Glu Val Glu Met Leu Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe
 210 215 220

Tyr Asp Ser Trp Lys Ser Val Leu Arg Gly Gln Val Cys Ile Val Leu
 225 230 235 240

Val Thr Glu Leu Met Thr Ser Gly Thr Leu Lys Thr Tyr Leu Arg Arg
 245 250 255

Phe Arg Glu Met Lys Pro Arg Val Leu Gln Arg Trp Ser Arg Gln Ile
 260 265 270

Leu Arg Gly Leu His Phe Leu His Ser Arg Val Pro Pro Ile Leu His
 275 280 285

Arg Asp Leu Lys Cys Asp Asn Val Phe Ile Thr Gly Pro Thr Gly Ser
 290 295 300

Val Lys Ile Gly Asp Leu Gly Leu Ala Thr Leu Lys Arg Ala Ser Phe
 305 310 315 320

Ala Lys Ser Val Ile Gly Thr Pro Glu Phe Met Ala Pro Glu Met Tyr
 325 330 335

Glu Glu Lys Tyr Asp Glu Ala Val Asp Val Tyr Ala Phe Gly Met Cys
 340 345 350

Met Leu Glu Met Ala Thr Ser Glu Tyr Pro Tyr Ser Glu Cys Gln Asn
 355 360 365

Ala Ala Gln Ile Tyr Arg Lys Val Thr Ser Gly Arg Lys Pro Asn Ser
 370 375 380

Phe His Lys Val Lys Ile Pro Glu Val Lys Glu Ile Ile Glu Gly Cys
385 390 395 400

Ile Arg Thr Asp Lys Asn Glu Arg Phe Thr Ile Gln Asp Leu Leu Ala
405 410 415

His Ala Phe Phe Arg Glu Glu Arg Gly Val His Val Glu Leu Ala Glu
420 425 430

Glu Asp Asp Gly Glu Lys Pro Gly Leu Lys Leu Trp Leu Arg Met Glu
435 440 445

Asp Ala Arg Arg Gly Gly Arg Pro Arg Asp Asn Gln Ala Ile Glu Phe
450 455 460

Leu Phe Gln Leu Gly Arg Asp Ala Ala Glu Glu Val Ala Gln Glu Met
465 470 475 480

Val Ala Leu Gly Leu Val Cys Glu Ala Asp Tyr Gln Pro Val Ala Arg
485 490 495

Ala Val Arg Glu Arg Val Ala Ala Ile Gln Arg Lys Arg Glu Lys Leu
500 505 510

Arg Lys Ala Arg Glu Leu Glu Ala Leu Pro Pro Glu Pro Gly Pro Pro
515 520 525

Pro Ala Thr Val Pro Met Ala Pro Gly Pro Pro Ser Val Phe Pro Pro
530 535 540

Glu Pro Glu Glu Pro Glu Ala Asp Gln His Gln Pro Phe Leu Phe Arg
545 550 555 560

His Ala Ser Tyr Ser Ser Thr Thr Ser Asp Cys Glu Thr Asp Gly Tyr
565 570 575

Leu Ser Ser Ser Gly Phe Leu Asp Ala Ser Asp Pro Ala Leu Gln Pro
580 585 590

Pro Gly Gly Val Pro Ser Ser Leu Ala Glu Ser His Leu Cys Leu Pro
595 600 605

Ser Ala Phe Ala Leu Ser Ile Pro Arg Ser Gly Pro Gly Ser Asp Phe
610 615 620

Ser Pro Gly Asp Ser Tyr Ala Ser Asp Ala Ala Ser Gly Leu Ser Asp
625 630 635 640

Val Gly Glu Gly Met Gly Gln Met Arg Arg Pro Pro Gly Arg Asn Leu
645 650 655

Arg Arg Arg Pro Arg Ser Arg Leu Arg Val Thr Ser Val Ser Asp Gln
660 665 670

Asn Asp Arg Val Val Glu Cys Gln Leu Gln Thr His Asn Ser Lys Met
675 680 685

Val Thr Phe Arg Phe Asp Leu Asp Gly Asp Ser Pro Glu Glu Ile Ala
690 695 700

Ala Ala Met Val Tyr Asn Glu Phe Ile Leu Pro Ser Glu Arg Asp Gly
705 710 715 720

Phe Leu Arg Arg Ile Arg Glu Ile Ile Gln Arg Val Glu Thr Leu Leu
725 730 735

Lys Arg Asp Thr Gly Pro Met Glu Ala Ala Glu Asp Thr Leu Ser Pro
740 745 750

Gln Glu Glu Pro Ala Pro Leu Pro Ala Leu Pro Val Pro Leu Pro Asp
755 760 765

Pro Ser Asn Glu Glu Leu Gln Ser Ser Thr Ser Leu Glu His Arg Ser
770 775 780

Trp Thr Ala Phe Ser Thr Ser Ser Ser Pro Gly Thr Pro Leu Ser
785 790 795 800

Pro Gly Asn Pro Phe Ser Pro Gly Thr Pro Ile Ser Pro Gly Pro Ile
805 810 815

Phe Pro Ile Thr Ser Pro Pro Cys His Pro Ser Pro Ser Pro Phe Ser
820 825 830

Pro Ile Ser Ser Gln Val Ser Ser Asn Pro Ser Pro His Pro Thr Ser
835 840 845

Ser Pro Leu Pro Phe Ser Ser Ser Thr Pro Glu Phe Pro Val Pro Leu
850 855 860

Ser Gln Cys Pro Trp Ser Ser Leu Pro Thr Thr Ser Pro Pro Thr Phe
865 870 875 880

Ser Pro Thr Cys Ser Gln Val Thr Leu Ser Ser Pro Phe Phe Pro Pro
885 890 895

Cys Pro Ser Thr Ser Ser Phe Pro Ser Thr Thr Ala Ala Pro Leu Leu
900 905 910

Ser Leu Ala Ser Ala Phe Ser Leu Ala Val Met Thr Val Ala Gln Ser
915 920 925

Leu Leu Ser Pro Ser Pro Gly Leu Leu Ser Gln Ser Pro Pro Ala Pro
930 935 940

Pro Ser Pro Leu Pro Ser Leu Pro Leu Pro Pro Pro Val Ala Pro Gly
945 950 955 960

Gly Gln Glu Ser Pro Ser Pro His Thr Ala Glu Val Glu Ser Glu Ala
965 970 975

Ser Pro Pro Pro Ala Arg Pro Leu Pro Gly Glu Ala Arg Leu Ala Pro
980 985 990

Ile Ser Glu Glu Gly Lys Pro Gln Leu Val Gly Arg Phe Gln Val Thr
995 1000 1005

Ser Ser Lys Glu Pro Ala Glu Pro Leu Pro Leu Gln Pro Thr Ser Pro
1010 1015 1020

Thr Leu Ser Gly Ser Pro Lys Pro Ser Thr Pro Gln Leu Thr Ser Glu
1025 1030 1035 1040

Ser Ser Asp Thr Glu Asp Ser Ala Gly Gly Pro Glu Thr Arg Glu
1045 1050 1055

Ala Leu Ala Glu Ser Asp Arg Ala Ala Glu Gly Leu Gly Ala Gly Val
1060 1065 1070

Glu Glu Glu Gly Asp Asp Gly Lys Glu Pro Gln Val Gly Ser Pro
1075 1080 1085

Gln Pro Leu Ser His Pro Ser Pro Val Trp Met Asn Tyr Ser Tyr Ser
1090 1095 1100

Ser Leu Cys Leu Ser Ser Glu Glu Ser Gln Ser Ser Gly Glu Asp Glu
1105 1110 1115 1120

Glu Phe Trp Ala Glu Leu Gln Ser Leu Arg Gln Lys His Leu Ser Glu
1125 1130 1135

Val Glu Thr Leu Gln Thr Leu Gln Lys Lys Glu Ile Glu Asp Leu Tyr
1140 1145 1150

Ser Arg Leu Gly Lys Gln Pro Pro Pro Gly Ile Val Ala Pro Ala Ala
1155 1160 1165

Met Leu Ser Ser Arg Gln Arg Arg Leu Ser Lys Gly Ser Phe Pro Thr
1170 1175 1180

Ser Arg Arg Asn Ser Leu Gln Arg Ser Glu Pro Pro Gly Pro Gly Ile
1185 1190 1195 1200

Met Arg Arg Asn Ser Leu Ser Gly Ser Ser Thr Gly Ser Gln Glu Gln
1205 1210 1215

Arg Ala Ser Lys Gly Val Thr Phe Ala Gly Asp Val Gly Arg Met
1220 1225 1230

<210> 38

<211> 670

<212> PRT

<213> Homo sapiens

<400> 38

Met Ser Gly Gly Ala Ala Glu Lys Gln Ser Ser Thr Pro Gly Ser Leu
1 5 10 15

Phe Leu Ser Pro Pro Ala Pro Ala Pro Lys Asn Gly Ser Ser Ser Asp
20 25 30

Ser Ser Val Gly Glu Lys Leu Gly Ala Ala Ala Ala Asp Ala Val Thr
35 40 45

Gly Arg Thr Glu Glu Tyr Arg Arg Arg Arg His Thr Met Asp Lys Asp
50 55 60

Ser Arg Gly Ala Ala Ala Thr Thr Thr Thr Glu His Arg Phe Phe
65 70 75 80

Arg Arg Ser Val Ile Cys Asp Ser Asn Ala Thr Ala Leu Glu Leu Pro
85 90 95

Gly Leu Pro Leu Ser Leu Pro Gln Pro Ser Ile Pro Ala Ala Val Pro
100 105 110

Gln Ser Ala Pro Pro Glu Pro His Arg Glu Glu Thr Val Thr Ala Thr
115 120 125

Ala Thr Ser Gln Val Ala Gln Gln Pro Pro Ala Ala Ala Pro Gly
130 135 140

Glu Gln Ala Val Ala Gly Pro Ala Pro Ser Thr Val Pro Ser Ser Thr
145 150 155 160

Ser Lys Asp Arg Pro Val Ser Gln Pro Ser Leu Val Gly Ser Lys Glu
165 170 175

Glu Pro Pro Pro Ala Arg Ser Gly Ser Gly Gly Ser Ala Lys Glu
180 185 190

Pro Gln Glu Glu Arg Ser Gln Gln Asp Asp Ile Glu Glu Leu Glu
195 200 205

Thr Lys Ala Val Gly Met Ser Asn Asp Gly Arg Phe Leu Lys Phe Asp
210 215 220

Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Lys Gly Leu Asp
225 230 235 240

Thr Glu Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Asp Arg Lys
245 250 255

Leu Thr Lys Ser Glu Arg Gln Arg Phe Lys Glu Glu Ala Glu Met Leu
260 265 270

Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Glu
275 280 285

Ser Thr Val Lys Gly Lys Cys Ile Val Leu Val Thr Glu Leu Met
290 295 300

Thr Ser Gly Thr Leu Lys Thr Tyr Leu Lys Arg Phe Lys Val Met Lys
305 310 315 320

Ile Lys Val Leu Arg Ser Trp Cys Arg Gln Ile Leu Lys Gly Leu Gln
325 330 335

Phe Leu His Thr Arg Thr Pro Pro Ile Ile His Arg Asp Leu Lys Cys
340 345 350

Asp Asn Ile Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp
355 360 365

Leu Gly Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile
370 375 380

Gly Thr Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp
385 390 395 400

Glu Ser Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala
 405 410 415

 Thr Ser Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Tyr
 420 425 430

 Arg Arg Val Thr Ser Gly Val Lys Pro Ala Ser Phe Asp Lys Val Ala
 435 440 445

 Ile Pro Glu Val Lys Glu Ile Ile Glu Gly Cys Ile Arg Gln Asn Lys
 450 455 460

 Asp Glu Arg Tyr Ser Ile Lys Asp Leu Leu Asn His Ala Phe Phe Gln
 465 470 475 480

 Glu Glu Thr Gly Val Arg Val Glu Leu Ala Glu Glu Asp Asp Gly Glu
 485 490 495

 Lys Ile Ala Ile Lys Leu Trp Leu Arg Ile Glu Asp Ile Lys Lys Leu
 500 505 510

 Lys Gly Lys Tyr Lys Asp Asn Glu Ala Ile Glu Phe Ser Phe Asp Leu
 515 520 525

 Glu Arg Asp Val Pro Glu Asp Val Ala Gln Glu Met Val Glu Ser Gly
 530 535 540

 Tyr Val Cys Glu Gly Asp His Lys Thr Met Ala Lys Ala Ile Lys Asp
 545 550 555 560

 Arg Val Ser Leu Ile Lys Arg Lys Arg Glu Gln Arg Gln Leu Val Arg
 565 570 575

 Glu Glu Gln Glu Lys Lys Gln Glu Glu Ser Ser Leu Lys Gln Gln
 580 585 590

 Val Glu Gln Ser Ser Ala Ser Gln Thr Gly Ile Lys Gln Leu Pro Ser
 595 600 605

 Ala Ser Thr Gly Ile Pro Thr Ala Ser Thr Thr Ser Ala Ser Val Ser
 610 615 620

 Thr Gln Val Glu Pro Glu Glu Pro Glu Ala Asp Gln His Gln Gln Leu
 625 630 635 640

 Gln Tyr Gln Gln Pro Ser Ile Ser Val Leu Ser Asp Gly Thr Val Asp
 645 650 655

Ser Gly Gln Gly Ser Ser Val Phe Thr Glu Ser Arg Gly Gly
660 665 670

<210> 39
<211> 2126
<212> PRT
<213> Rattus norvegicus

<400> 39
Met Ser Asp Gly Thr Ala Glu Lys Gln Ser Gly Thr Pro Gly Phe Leu
1 5 10 15

Ser Pro Pro Ala Pro Val Pro Lys Asn Gly Ser Ser Ser Asp Ser Ser
20 25 30

Val Gly Glu Lys Leu Gly Ala Ala Val Ala Asp Ser Gly Ile Gly Arg
35 40 45

Thr Glu Glu Tyr Arg Arg Arg Arg His Thr Met Asp Lys Asp Ser Arg
50 55 60

Gly Ala Ala Ala Thr Thr Pro Thr Glu His Arg Phe Phe Arg Arg
65 70 75 80

Ser Val Ile Cys Asp Ser Asn Ala Thr Ala Leu Glu Leu Pro Gly Leu
85 90 95

Pro Leu Ser Ile Pro Gln Pro Ser Val Pro Ala Val Val Pro Gln Ser
100 105 110

Ala Pro Pro Glu Pro His Arg Glu Glu Thr Leu Thr Ala Thr Val Ala
115 120 125

Ser Gln Val Ser Gln Gln Pro Ser Ala Ala Ala Ser Pro Gly Glu Gln
130 135 140

Ala Val Val Gly Ser Ala Thr Ala Thr Val Pro Ser Ser Thr Ser Lys
145 150 155 160

Asp Arg Pro Val Ser Gln Pro Ser Leu Val Gly Ser Lys Glu Glu Pro
165 170 175

Pro Pro Ser Arg Ser Gly Ser Gly Gly Ala Ser Ala Lys Glu
180 185 190

Pro Gln Glu Glu Arg Asn Gln Gln Asp Asp Ile Glu Glu Leu Glu

195	200	205
Thr Lys Ala Val Gly Met Ser Asn Asp Gly Arg Phe Leu Lys Phe Asp		
210	215	220
Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Lys Gly Leu Asp		
225	230	235
240		
Thr Glu Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Asp Arg Lys		
245	250	255
Leu Thr Lys Ser Glu Arg Gln Arg Phe Lys Glu Glu Ala Glu Met Leu		
260	265	270
Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Glu		
275	280	285
Ser Thr Val Lys Gly Lys Lys Cys Ile Val Leu Val Thr Glu Leu Met		
290	295	300
Thr Ser Gly Thr Leu Lys Thr Tyr Leu Lys Arg Phe Lys Val Met Lys		
305	310	315
320		
Ile Lys Val Leu Arg Ser Trp Cys Arg Gln Ile Leu Lys Gly Leu Gln		
325	330	335
Phe Leu His Thr Arg Thr Pro Pro Ile Ile His Arg Asp Leu Lys Cys		
340	345	350
Asp Asn Ile Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp		
355	360	365
Leu Gly Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile		
370	375	380
Gly Thr Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp		
385	390	395
400		
Glu Ser Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala		
405	410	415
Thr Ser Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Tyr		
420	425	430
Arg Arg Val Thr Ser Gly Val Lys Pro Ala Ser Phe Asp Lys Val Ala		
435	440	445
Ile Pro Glu Val Lys Glu Ile Ile Glu Gly Cys Ile Arg Gln Asn Lys		

450	455	460
Asp Glu Arg Tyr Ser Ile Lys Asp Leu Leu Asn His Ala Phe Phe Gln		
465	470	475
Glu Glu Thr Gly Val Arg Val Glu Leu Ala Glu Glu Asp Asp Gly Glu		
485	490	495
Lys Ile Ala Ile Lys Leu Trp Leu Arg Ile Glu Asp Ile Lys Lys Leu		
500	505	510
Lys Gly Lys Tyr Lys Asp Asn Glu Ala Ile Glu Phe Ser Phe Asp Leu		
515	520	525
Glu Arg Asp Val Pro Glu Asp Val Ala Gln Glu Met Val Glu Ser Gly		
530	535	540
Tyr Val Cys Glu Gly Asp His Lys Thr Met Ala Lys Ala Ile Lys Asp		
545	550	555
560		
Arg Val Ser Leu Ile Lys Arg Lys Arg Glu Gln Arg Gln Leu Val Arg		
565	570	575
Glu Glu Gln Glu Lys Arg Lys Gln Glu Glu Ser Ser Phe Lys Gln Gln		
580	585	590
Asn Glu Gln Gln Ala Ser Val Ser Gln Ala Gly Ile Gln Pro Leu Ser		
595	600	605
Val Ala Ser Thr Gly Ile Pro Thr Ala Pro Thr Thr Ser Ala Ser Val		
610	615	620
Ser Thr Gln Val Glu Pro Glu Glu Pro Glu Ala Asp Gln His Gln Gln		
625	630	635
640		
Leu Gln Tyr Gln Gln Pro Ser Ile Ser Val Leu Ser Asp Gly Thr Val		
645	650	655
Asp Ser Gly Gln Gly Ser Ser Val Phe Thr Glu Ser Arg Val Ser Ser		
660	665	670
Gln Gln Thr Val Ser Tyr Gly Ser Gln His Glu Gln Ala His Ser Ile		
675	680	685
Gly Thr Ala Pro Gly His Thr Val Ser Ser Ile Gln Ala Gln Ser Gln		
690	695	700
Pro His Gly Val Tyr Pro Pro Ser Ser Met Ala Gln Gly Gln Asn Gln		

705	710	715	720
Gly Gln Pro Ser Ser Ser Leu Ala Gly Val Leu Ser Ser Gln Pro Val			
725	730	735	
Gln His Pro Gln Gln Gly Ile Gln Pro Thr Val Pro Pro Gln Gln			
740	745	750	
Ala Val Gln Tyr Ser Leu Pro Gln Ala Ala Ser Ser Ser Glu Gly Thr			
755	760	765	
Val Gln Pro Val Ser Gln Pro Gln Val Ser Ala Gly Thr Gln Ser Ser			
770	775	780	
Thr Gln Gly Val Ser Gln Ala Ala Pro Pro Glu Gln Thr Pro Ile Thr			
785	790	795	800
Gln Ser Gln Pro Thr Gln Pro Val Pro Leu Val Ser Ser Val Asp Ser			
805	810	815	
Ala His Ser Asp Val Ala Ser Gly Met Ser Asp Gly Asn Glu Asn Ala			
820	825	830	
Pro Ser Ser Ser Gly Arg His Glu Gly Arg Thr Thr Lys Arg His Tyr			
835	840	845	
Arg Lys Ser Val Arg Ser Arg Ser Arg His Glu Lys Thr Ser Arg Pro			
850	855	860	
Lys Leu Arg Ile Leu Asn Val Ser Asn Lys Gly Asp Arg Val Val Glu			
865	870	875	880
Cys Gln Leu Glu Thr His Asn Arg Lys Met Val Thr Phe Lys Phe Asp			
885	890	895	
Leu Asp Gly Asp Asn Pro Glu Glu Ile Ala Thr Ile Met Val Asn Asn			
900	905	910	
Asp Phe Ile Leu Ala Ile Glu Arg Glu Ser Phe Val Ala Gln Val Arg			
915	920	925	
Glu Ile Ile Glu Lys Ala Asp Glu Met Leu Ser Glu Asp Val Ser Val			
930	935	940	
Glu Pro Glu Gly Asp Gln Gly Leu Glu Ser Leu Gln Gly Lys Asp Asp			
945	950	955	960
Tyr Gly Phe Pro Gly Ser Gln Lys Leu Glu Gly Glu Phe Lys Gln Pro			

965	970	975
Ile Ala Val Ser Ser Met Pro Gln Gln Ile Gly Val Pro Thr Ser Ser		
980	985	990
Leu Thr Gln Val Val His Ser Ala Gly Arg Arg Phe Ile Val Ser Pro		
995	1000	1005
Val Pro Glu Ser Arg Leu Arg Glu Ser Lys Ile Phe Thr Ser Glu Ile		
1010	1015	1020
Pro Asp Pro Val Ala Ala Ser Thr Ser Gln Gly Pro Gly Met Asn Leu		
1025	1030	1035
Ser His Ser Ala Ser Ser Leu Ser Leu Gln Gln Ala Phe Ser Glu Leu		
1045	1050	1055
Lys His Gly Gln Met Thr Glu Gly Pro Asn Thr Ala Pro Pro Asn Phe		
1060	1065	1070
Asn His Pro Gly Pro Thr Phe Ser Pro Phe Leu Thr Ser Ile Ala Gly		
1075	1080	1085
Val Gln Thr Val Ala Ala Ser Thr Pro Ser Val Ser Val Pro Ile Thr		
1090	1095	1100
Ser Ser Pro Leu Asn Asp Ile Ser Thr Ser Val Met Gln Ser Glu Gly		
1105	1110	1115
Ala Leu Pro Thr Asp Lys Gly Ile Gly Gly Val Thr Thr Ser Thr Gly		
1125	1130	1135
Val Val Ala Ser Gly Gly Leu Thr Thr Leu Ser Val Ser Glu Thr Pro		
1140	1145	1150
Thr Leu Ser Ser Ala Val Ser Ser Ser Thr Ala Pro Ala Val Val Thr		
1155	1160	1165
Val Ser Thr Thr Ser Gln Pro Val Gln Ala Phe Thr Ser Gly Ser Ile		
1170	1175	1180
Ala Ser Ser Thr Gly Ser Phe Pro Ser Gly Thr Phe Ser Thr Thr Thr		
1185	1190	1195
Gly Thr Thr Val Ser Ser Val Ala Val Pro Asn Ala Lys Pro Pro Thr		
1205	1210	1215
Val Leu Leu Gln Gln Val Ala Gly Asn Thr Ala Gly Val Ala Ile Val		

1220	1225	1230
Thr Ser Val Ser Thr Thr Pro Phe Pro Ala Met Ala Ser Gln Pro		
1235	1240	1245
Ser Leu Pro Leu Gly Ser Ser Thr Ser Ala Pro Thr Leu Ala Glu Thr		
1250	1255	1260
Val Val Val Ser Ala His Ser Leu Asp Lys Ala Ser His Ser Ser Thr		
1265	1270	1275
Ala Gly Leu Gly Leu Ser Phe Cys Ala Pro Ser Ser Ser Ser Ser		
1285	1290	1295
Gly Thr Ala Val Ser Ser Ser Val Ser Gln Pro Gly Ile Val His Pro		
1300	1305	1310
Leu Val Ile Ser Ser Ala Ile Ala Ser Thr Pro Val Leu Pro Gln Pro		
1315	1320	1325
Ala Val Pro Thr Ser Thr Pro Leu Leu Pro Gln Val Pro Asn Ile Pro		
1330	1335	1340
Pro Leu Val Gln Pro Val Ala Asn Val Pro Ala Val Gln Gln Thr Leu		
1345	1350	1355
Ile His Ser Gln Pro Gln Pro Ala Leu Leu Pro Asn Gln Pro His Thr		
1365	1370	1375
His Cys Pro Glu Met Asp Ala Asp Thr Gln Ser Lys Ala Pro Gly Ile		
1380	1385	1390
Asp Asp Ile Lys Thr Leu Glu Glu Lys Leu Arg Ser Leu Phe Ser Glu		
1395	1400	1405
His Ser Ser Ser Gly Thr Gln His Ala Ser Val Ser Leu Glu Thr Pro		
1410	1415	1420
Leu Val Val Glu Thr Val Thr Pro Gly Ile Pro Thr Thr Ala Val Ala		
1425	1430	1435
Pro Ser Lys Leu Met Thr Ser Thr Ser Thr Cys Leu Pro Pro Thr		
1445	1450	1455
Asn Leu Pro Leu Gly Thr Ala Gly Met Pro Val Met Pro Val Gly Thr		
1460	1465	1470
Pro Gly Gln Val Ser Thr Pro Gly Thr His Ala Ser Ala Pro Ala Ser		

1475	1480	1485
Thr Ala Thr Gly Ala Lys Pro Gly Thr Thr Pro Pro Lys Pro Ser Leu		
1490	1495	1500
Thr Lys Thr Val Val Pro Pro Val Gly Thr Glu Leu Ser Ala Gly Thr		
1505	1510	1515
Val Pro Cys Glu Gln Leu Pro Pro Phe Pro Gly Pro Ser Leu Ile Gln		
1525	1530	1535
Thr Gln Gln Pro Leu Glu Asp Leu Asp Ala Gln Leu Arg Arg Thr Leu		
1540	1545	1550
Ser Pro Glu Thr Ile Pro Val Thr Pro Ala Val Gly Pro Leu Ser Thr		
1555	1560	1565
Met Ser Ser Thr Ala Val Thr Glu Ala Gly Ser Gln Pro Gln Lys Asp		
1570	1575	1580
Gly Thr Glu Val His Val Thr Ala Ser Ser Gly Ala Gly Val Val		
1585	1590	1595
1600		
Lys Met Gly Arg Phe Gln Val Ser Val Thr Met Asp Asp Ala Gln Lys		
1605	1610	1615
Glu Arg Lys Asn Arg Ser Glu Asp Thr Lys Ser Val His Phe Glu Ser		
1620	1625	1630
Ser Thr Ser Glu Ser Ser Val Leu Ser Ser Ser Pro Glu Ser Thr		
1635	1640	1645
Leu Val Lys Pro Glu Pro Asn Gly Ile Thr Val Ser Gly Ile Ser Leu		
1650	1655	1660
Asp Val Pro Asp Ser Thr His Arg Thr Pro Thr Pro Glu Ala Lys Ser		
1665	1670	1675
1680		
Glu Thr Gly Gln Pro Thr Lys Val Gly Arg Phe Gln Val Thr Thr Thr		
1685	1690	1695
Ala Asn Lys Val Gly Arg Phe Ser Val Ser Arg Thr Glu Asp Lys Val		
1700	1705	1710
Thr Glu Leu Lys Lys Glu Gly Pro Val Thr Ser Pro Phe Arg Asp Ser		
1715	1720	1725
Glu Gln Thr Val Ile Pro Ala Ala Ile Pro Lys Lys Glu Lys Pro Glu		

1730

1735

1740

Leu Ala Glu Pro Ser His Leu Asn Gly Pro Ser Ser Asp Leu Glu Ala
1745 1750 1755 1760

Ala Phe Leu Ser Arg Gly Gly Glu Asp Gly Ser Gly Ser Pro His Ser
1765 1770 1775

Pro Pro His Leu Cys Ser Lys Ser Leu Pro Ile Gln Thr Leu Ser Gln
1780 1785 1790

Ser Leu Ser Asn Ser Phe Asn Ser Ser Tyr Met Ser Ser Asp Asn Glu
1795 1800 1805

Ser Asp Ile Glu Asp Glu Asp Leu Arg Leu Glu Leu Arg Arg Leu Arg
1810 1815 1820

Glu Lys His Leu Lys Glu Ile Gln Asp Leu Gln Ser Arg Gln Lys His
1825 1830 1835 1840

Glu Ile Glu Ser Leu Tyr Thr Lys Leu Gly Lys Val Pro Pro Ala Val
1845 1850 1855

Ile Ile Pro Pro Ala Ala Pro Leu Ser Gly Arg Arg Arg Arg Pro Thr
1860 1865 1870

Lys Ser Lys Gly Ser Lys Ser Ser Arg Ser Ser Leu Gly Asn Lys
1875 1880 1885

Ser Pro Gln Leu Ser Gly Asn Leu Ser Gly Gln Ser Gly Thr Ser Val
1890 1895 1900

Leu Asn Pro Gln Gln Thr Leu His Pro Pro Gly Asn Thr Pro Glu Thr
1905 1910 1915 1920

Gly His Asn Gln Leu Leu Gln Pro Leu Lys Pro Ser Pro Ser Ser Asp
1925 1930 1935

Asn Leu Tyr Ser Ala Phe Thr Ser Asp Gly Ala Ile Ser Ile Pro Ser
1940 1945 1950

Leu Ser Ala Pro Gly Gln Gly Thr Ser Ser Thr Asn Thr Val Gly Gly
1955 1960 1965

Thr Val Ser Ser Gln Ala Ala Gln Ala Gln Pro Pro Ala Met Thr Ser
1970 1975 1980

Ser Arg Lys Gly Thr Phe Thr Asp Asp Leu His Lys Leu Val Asp Asn

1985	1990	1995	2000
Trp Ala Arg Asp Ala Met Asn Leu Ser Gly Arg Arg Gly Ser Lys Gly			
2005	2010	2015	
His Met Asn Tyr Glu Gly Pro Gly Met Ala Arg Lys Phe Ser Ala Pro			
2020	2025	2030	
Gly Gln Leu Cys Ile Ser Met Thr Ser Asn Met Gly Gly Ser Thr Pro			
2035	2040	2045	
Ile Ser Ala Ala Ser Ala Thr Ser Leu Gly His Phe Thr Lys Ser Met			
2050	2055	2060	
Cys Pro Pro Gln Gln Tyr Gly Phe Pro Ala Ala Pro Phe Gly Thr Gln			
2065	2070	2075	2080
Trp Ser Gly Thr Gly Gly Pro Ala Pro Gln Pro Leu Gly Gln Phe Gln			
2085	2090	2095	
Pro Val Gly Thr Thr Ser Leu Gln Asn Phe Asn Ile Ser Asn Leu Gln			
2100	2105	2110	
Lys Ser Ile Ser Asn Pro Pro Ser Ser Asn Leu Arg Thr Thr			
2115	2120	2125	
<210> 40			
<211> 2382			
<212> PRT			
<213> Homo sapiens			
<400> 40			
Met Ser Gly Gly Ala Ala Glu Lys Gln Ser Ser Thr Pro Gly Ser Leu			
1	5	10	15
Phe Leu Ser Pro Pro Ala Pro Ala Pro Lys Asn Gly Ser Ser Ser Asp			
20	25	30	
Ser Ser Val Gly Glu Lys Leu Gly Ala Ala Ala Ala Asp Ala Val Thr			
35	40	45	
Gly Arg Thr Glu Glu Tyr Arg Arg Arg Arg His Thr Met Asp Lys Asp			
50	55	60	
Ser Arg Gly Ala Ala Ala Thr Thr Thr Thr Glu His Arg Phe Phe			
65	70	75	80

Arg Arg Ser Val Ile Cys Asp Ser Asn Ala Thr Ala Leu Glu Leu Pro
85 90 95

Gly Leu Pro Leu Ser Leu Pro Gln Pro Ser Ile Pro Ala Ala Val Pro
100 105 110

Gln Ser Ala Pro Pro Glu Pro His Arg Glu Glu Thr Val Thr Ala Thr
115 120 125

Ala Thr Ser Gln Val Ala Gln Gln Pro Pro Ala Ala Ala Ala Pro Gly
130 135 140

Glu Gln Ala Val Ala Gly Pro Ala Pro Ser Thr Val Pro Ser Ser Thr
145 150 155 160

Ser Lys Asp Arg Pro Val Ser Gln Pro Ser Leu Val Gly Ser Lys Glu
165 170 175

Glu Pro Pro Pro Ala Arg Ser Gly Ser Gly Gly Ser Ala Lys Glu
180 185 190

Pro Gln Glu Glu Arg Ser Gln Gln Asp Asp Ile Glu Glu Leu Glu
195 200 205

Thr Lys Ala Val Gly Met Ser Asn Asp Gly Arg Phe Leu Lys Phe Asp
210 215 220

Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Lys Gly Leu Asp
225 230 235 240

Thr Glu Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Asp Arg Lys
245 250 255

Leu Thr Lys Ser Glu Arg Gln Arg Phe Lys Glu Glu Ala Glu Met Leu
260 265 270

Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Glu
275 280 285

Ser Thr Val Lys Gly Lys Lys Cys Ile Val Leu Val Thr Glu Leu Met
290 295 300

Thr Ser Gly Thr Leu Lys Thr Tyr Leu Lys Arg Phe Lys Val Met Lys
305 310 315 320

Ile Lys Val Leu Arg Ser Trp Cys Arg Gln Ile Leu Lys Gly Leu Gln
325 330 335

Phe Leu His Thr Arg Thr Pro Pro Ile Ile His Arg Asp Leu Lys Cys
340 345 350

Asp Asn Ile Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Ile Gly Asp
355 360 365

Leu Gly Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile
370 375 380

Gly Thr Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp
385 390 395 400

Glu Ser Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala
405 410 415

Thr Ser Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Tyr
420 425 430

Arg Arg Val Thr Ser Gly Val Lys Pro Ala Ser Phe Asp Lys Val Ala
435 440 445

Ile Pro Glu Val Lys Glu Ile Ile Glu Gly Cys Ile Arg Gln Asn Lys
450 455 460

Asp Glu Arg Tyr Ser Ile Lys Asp Leu Leu Asn His Ala Phe Phe Gln
465 470 475 480

Glu Glu Thr Gly Val Arg Val Glu Leu Ala Glu Glu Asp Asp Gly Glu
485 490 495

Lys Ile Ala Ile Lys Leu Trp Leu Arg Ile Glu Asp Ile Lys Lys Leu
500 505 510

Lys Gly Lys Tyr Lys Asp Asn Glu Ala Ile Glu Phe Ser Phe Asp Leu
515 520 525

Glu Arg Asp Val Pro Glu Asp Val Ala Gln Glu Met Val Glu Ser Gly
530 535 540

Tyr Val Cys Glu Gly Asp His Lys Thr Met Ala Lys Ala Ile Lys Asp
545 550 555 560

Arg Val Ser Leu Ile Lys Arg Lys Arg Glu Gln Arg Gln Leu Val Arg
565 570 575

Glu Glu Gln Glu Lys Lys Gln Glu Glu Ser Ser Leu Lys Gln Gln
580 585 590

Val Glu Gln Ser Ser Ala Ser Gln Thr Gly Ile Lys Gln Leu Pro Ser
595 600 605

Ala Ser Thr Gly Ile Pro Thr Ala Ser Thr Thr Ser Ala Ser Val Ser
610 615 620

Thr Gln Val Glu Pro Glu Glu Pro Glu Ala Asp Gln His Gln Gln Leu
625 630 635 640

Gln Tyr Gln Gln Pro Ser Ile Ser Val Leu Ser Asp Gly Thr Val Asp
645 650 655

Ser Gly Gln Gly Ser Ser Val Phe Thr Glu Ser Arg Val Ser Ser Gln
660 665 670

Gln Thr Val Ser Tyr Gly Ser Gln His Glu Gln Ala His Ser Thr Gly
675 680 685

Thr Val Pro Gly His Ile Pro Ser Thr Val Gln Ala Gln Ser Gln Pro
690 695 700

His Gly Val Tyr Pro Pro Ser Ser Val Ala Gln Gly Gln Ser Gln Gly
705 710 715 720

Gln Pro Ser Ser Ser Ser Leu Thr Gly Val Ser Ser Ser Gln Pro Ile
725 730 735

Gln His Pro Gln Gln Gln Gly Ile Gln Gln Thr Ala Pro Pro Gln
740 745 750

Gln Thr Val Gln Tyr Ser Leu Ser Gln Thr Ser Thr Ser Ser Glu Ala
755 760 765

Thr Thr Ala Gln Pro Val Ser Gln Pro Gln Ala Pro Gln Val Leu Pro
770 775 780

Gln Val Ser Ala Gly Lys Gln Leu Pro Val Ser Gln Pro Val Pro Thr
785 790 795 800

Ile Gln Gly Glu Pro Gln Ile Pro Val Ala Thr Gln Pro Ser Val Val
805 810 815

Pro Val His Ser Gly Ala His Phe Leu Pro Val Gly Gln Pro Leu Pro
820 825 830

Thr Pro Leu Leu Pro Gln Tyr Pro Val Ser Gln Ile Pro Ile Ser Thr
835 840 845

Pro His Val Ser Thr Ala Gln Thr Gly Phe Ser Ser Leu Pro Ile Thr
850 855 860

Met Ala Ala Gly Ile Thr Gln Pro Leu Leu Thr Leu Ala Ser Ser Ala
865 870 875 880

Thr Thr Ala Ala Ile Pro Gly Val Ser Thr Val Val Pro Ser Gln Leu
885 890 895

Pro Thr Leu Leu Gln Pro Val Thr Gln Leu Pro Ser Gln Val His Pro
900 905 910

Gln Leu Leu Gln Pro Ala Val Gln Ser Met Gly Ile Pro Ala Asn Leu
915 920 925

Gly Gln Ala Ala Glu Val Pro Leu Ser Ser Gly Asp Val Leu Tyr Gln
930 935 940

Gly Phe Pro Pro Arg Leu Pro Pro Gln Tyr Pro Gly Asp Ser Asn Ile
945 950 955 960

Ala Pro Ser Ser Asn Val Ala Ser Val Cys Ile His Ser Thr Val Leu
965 970 975

Ser Pro Pro Met Pro Thr Glu Val Leu Ala Thr Pro Gly Tyr Phe Pro
980 985 990

Thr Val Val Gln Pro Tyr Val Glu Ser Asn Leu Leu Val Pro Met Gly
995 1000 1005

Gly Val Gly Gly Gln Val Gln Val Ser Gln Pro Gly Gly Ser Leu Ala
1010 1015 1020

Gln Ala Pro Thr Thr Ser Ser Gln Gln Ala Val Leu Glu Ser Thr Gln
1025 1030 1035 1040

Gly Val Ser Gln Val Ala Pro Ala Glu Pro Val Ala Val Ala Gln Pro
1045 1050 1055

Gln Ala Thr Gln Pro Thr Thr Leu Ala Ser Ser Val Asp Ser Ala His
1060 1065 1070

Ser Asp Val Ala Ser Gly Met Ser Asp Gly Asn Glu Asn Val Pro Ser
1075 1080 1085

Ser Ser Gly Arg His Glu Gly Arg Thr Thr Lys Arg His Tyr Arg Lys
1090 1095 1100

Ser Val Arg Ser Arg Ser Arg His Glu Lys Thr Ser Arg Pro Lys Leu
1105 1110 1115 1120

Arg Ile Leu Asn Val Ser Asn Lys Gly Asp Arg Val Val Glu Cys Gln
1125 1130 1135

Leu Glu Thr His Asn Arg Lys Met Val Thr Phe Lys Phe Asp Leu Asp
1140 1145 1150

Gly Asp Asn Pro Glu Glu Ile Ala Thr Ile Met Val Asn Asn Asp Phe
1155 1160 1165

Ile Leu Ala Ile Glu Arg Glu Ser Phe Val Asp Gln Val Arg Glu Ile
1170 1175 1180

Ile Glu Lys Ala Asp Glu Met Leu Ser Glu Asp Val Ser Val Glu Pro
1185 1190 1195 1200

Glu Gly Asp Gln Gly Leu Glu Ser Leu Gln Gly Lys Asp Asp Tyr Gly
1205 1210 1215

Phe Ser Gly Ser Gln Lys Leu Glu Gly Glu Phe Lys Gln Pro Ile Pro
1220 1225 1230

Ala Ser Ser Met Pro Gln Gln Ile Gly Ile Pro Thr Ser Ser Leu Thr
1235 1240 1245

Gln Val Val His Ser Ala Gly Arg Arg Phe Ile Val Ser Pro Val Pro
1250 1255 1260

Glu Ser Arg Leu Arg Glu Ser Lys Val Phe Pro Ser Glu Ile Thr Asp
1265 1270 1275 1280

Thr Val Ala Ala Ser Thr Ala Gln Ser Pro Gly Met Asn Leu Ser His
1285 1290 1295

Ser Ala Ser Ser Leu Ser Leu Gln Gln Ala Phe Ser Glu Leu Arg Arg
1300 1305 1310

Ala Gln Met Thr Glu Gly Pro Asn Thr Ala Pro Pro Asn Phe Ser His
1315 1320 1325

Thr Gly Pro Thr Phe Pro Val Val Pro Pro Phe Leu Ser Ser Ile Ala
1330 1335 1340

Gly Val Pro Thr Thr Ala Ala Ala Thr Ala Pro Val Pro Ala Thr Ser
1345 1350 1355 1360

Ser Pro Pro Asn Asp Ile Ser Thr Ser Val Ile Gln Ser Glu Val Thr
1365 1370 1375

Val Pro Thr Glu Glu Gly Ile Ala Gly Val Ala Thr Ser Thr Gly Val
1380 1385 1390

Val Thr Ser Gly Gly Leu Pro Ile Pro Pro Val Ser Glu Ser Pro Val
1395 1400 1405

Leu Ser Ser Val Val Ser Ser Ile Thr Ile Pro Ala Val Val Ser Ile
1410 1415 1420

Ser Thr Thr Ser Pro Ser Leu Gln Val Pro Thr Ser Thr Ser Glu Ile
1425 1430 1435 1440

Val Val Ser Ser Thr Ala Leu Tyr Pro Ser Val Thr Val Ser Ala Thr
1445 1450 1455

Ser Ala Ser Ala Gly Gly Ser Thr Ala Thr Pro Gly Pro Lys Pro Pro
1460 1465 1470

Ala Val Val Ser Gln Gln Ala Ala Gly Ser Thr Thr Val Gly Ala Thr
1475 1480 1485

Leu Thr Ser Val Ser Thr Thr Ser Phe Pro Ser Thr Ala Ser Gln
1490 1495 1500

Leu Ser Ile Gln Leu Ser Ser Ser Thr Ser Thr Pro Thr Leu Ala Glu
1505 1510 1515 1520

Thr Val Val Val Ser Ala His Ser Leu Asp Lys Thr Ser His Ser Ser
1525 1530 1535

Thr Thr Gly Leu Ala Phe Ser Leu Ser Ala Pro Ser Ser Ser Ser
1540 1545 1550

Pro Gly Ala Gly Val Ser Ser Tyr Ile Ser Gln Pro Gly Gly Leu His
1555 1560 1565

Pro Leu Val Ile Pro Ser Val Ile Ala Ser Thr Pro Ile Leu Pro Gln
1570 1575 1580

Ala Ala Gly Pro Thr Ser Thr Pro Leu Leu Pro Gln Val Pro Ser Ile
1585 1590 1595 1600

Pro Pro Leu Val Gln Pro Val Ala Asn Val Pro Ala Val Gln Gln Thr
1605 1610 1615

Leu Ile His Ser Gln Pro Gln Pro Ala Leu Leu Pro Asn Gln Pro His
1620 1625 1630

Thr His Cys Pro Glu Val Asp Ser Asp Thr Gln Pro Lys Ala Pro Gly
1635 1640 1645

Ile Asp Asp Ile Lys Thr Leu Glu Glu Lys Leu Arg Ser Leu Phe Ser
1650 1655 1660

Glu His Ser Ser Ser Gly Ala Gln His Ala Ser Val Ser Leu Glu Thr
1665 1670 1675 1680

Ser Leu Val Ile Glu Ser Thr Val Thr Pro Gly Ile Pro Thr Thr Ala
1685 1690 1695

Val Ala Pro Ser Lys Leu Leu Thr Ser Thr Ser Thr Cys Leu Pro
1700 1705 1710

Pro Thr Asn Leu Pro Leu Gly Thr Val Ala Leu Pro Val Thr Pro Val
1715 1720 1725

Val Thr Pro Gly Gln Val Ser Thr Pro Val Ser Thr Thr Ser Gly
1730 1735 1740

Val Lys Pro Gly Thr Ala Pro Ser Lys Pro Pro Leu Thr Lys Ala Pro
1745 1750 1755 1760

Val Leu Pro Val Gly Thr Glu Leu Pro Ala Gly Thr Leu Pro Ser Glu
1765 1770 1775

Gln Leu Pro Pro Phe Pro Gly Pro Ser Leu Thr Gln Ser Gln Pro
1780 1785 1790

Leu Glu Asp Leu Asp Ala Gln Leu Arg Arg Thr Leu Ser Pro Glu Ile
1795 1800 1805

Ile Thr Val Thr Ser Ala Val Gly Pro Val Ser Met Ala Ala Pro Thr
1810 1815 1820

Ala Ile Thr Glu Ala Gly Thr Gln Pro Gln Lys Gly Val Ser Gln Val
1825 1830 1835 1840

Lys Glu Gly Pro Val Leu Ala Thr Ser Ser Gly Ala Gly Val Phe Lys
1845 1850 1855

Met Gly Arg Phe Gln Val Ser Val Ala Ala Asp Gly Ala Gln Lys Glu
1860 1865 1870

Gly Lys Asn Lys Ser Glu Asp Ala Lys Ser Val His Phe Glu Ser Ser
1875 1880 1885

Thr Ser Glu Ser Ser Val Leu Ser Ser Ser Pro Glu Ser Thr Leu
1890 1895 1900

Val Lys Pro Glu Pro Asn Gly Ile Thr Ile Pro Gly Ile Ser Ser Asp
1905 1910 1915 1920

Val Pro Glu Ser Ala His Lys Thr Thr Ala Ser Glu Ala Lys Ser Asp
1925 1930 1935

Thr Gly Gln Pro Thr Lys Val Gly Arg Phe Gln Val Thr Thr Ala
1940 1945 1950

Asn Lys Val Gly Arg Phe Ser Val Ser Lys Thr Glu Asp Lys Ile Thr
1955 1960 1965

Asp Thr Lys Lys Glu Gly Pro Val Ala Ser Pro Pro Phe Met Asp Leu
1970 1975 1980

Glu Gln Ala Val Leu Pro Ala Val Ile Pro Lys Lys Glu Lys Pro Glu
1985 1990 1995 2000

Leu Ser Glu Pro Ser His Leu Asn Gly Pro Ser Ser Asp Pro Glu Ala
2005 2010 2015

Ala Phe Leu Ser Arg Asp Val Asp Asp Gly Ser Gly Ser Pro His Ser
2020 2025 2030

Pro His Gln Leu Ser Ser Lys Ser Leu Pro Ser Gln Asn Leu Ser Gln
2035 2040 2045

Ser Leu Ser Asn Ser Phe Asn Ser Ser Tyr Met Ser Ser Asp Asn Glu
2050 2055 2060

Ser Asp Ile Glu Asp Glu Asp Leu Lys Leu Glu Leu Arg Arg Leu Arg
2065 2070 2075 2080

Asp Lys His Leu Lys Glu Ile Gln Asp Leu Gln Ser Arg Gln Lys His
2085 2090 2095

Glu Ile Glu Ser Leu Tyr Thr Lys Leu Gly Lys Val Pro Pro Ala Val
2100 2105 2110

Ile Ile Pro Pro Ala Ala Pro Leu Ser Gly Arg Arg Arg Arg Pro Thr
2115 2120 2125

Lys Ser Lys Gly Ser Lys Ser Ser Arg Ser Ser Ser Leu Gly Asn Lys
2130 2135 2140

Ser Pro Gln Leu Ser Gly Asn Leu Ser Gly Gln Ser Ala Ala Ser Val
2145 2150 2155 2160

Leu His Pro Gln Gln Thr Leu His Pro Pro Gly Asn Ile Pro Glu Ser
2165 2170 2175

Gly Gln Asn Gln Leu Leu Gln Pro Leu Lys Pro Ser Pro Ser Ser Asp
2180 2185 2190

Asn Leu Tyr Ser Ala Phe Thr Ser Asp Gly Ala Ile Ser Val Pro Ser
2195 2200 2205

Leu Ser Ala Pro Gly Gln Gly Thr Ser Ser Thr Asn Thr Val Gly Ala
2210 2215 2220

Thr Val Asn Ser Gln Ala Ala Gln Ala Gln Pro Pro Ala Met Thr Ser
2225 2230 2235 2240

Ser Arg Lys Gly Thr Phe Thr Asp Asp Leu His Lys Leu Val Asp Asn
2245 2250 2255

Trp Ala Arg Asp Ala Met Asn Leu Ser Gly Arg Arg Gly Ser Lys Gly
2260 2265 2270

His Met Asn Tyr Glu Gly Pro Gly Met Ala Arg Lys Phe Ser Ala Pro
2275 2280 2285

Gly Gln Leu Cys Ile Ser Met Thr Ser Asn Leu Gly Gly Ser Ala Pro
2290 2295 2300

Ile Ser Ala Ala Ser Ala Thr Ser Leu Gly His Phe Thr Lys Ser Met
2305 2310 2315 2320

Cys Pro Pro Gln Gln Tyr Gly Phe Pro Ala Thr Pro Phe Gly Ala Gln
2325 2330 2335

Trp Ser Gly Thr Gly Gly Pro Ala Pro Gln Pro Leu Gly Gln Phe Gln
2340 2345 2350

Pro Val Gly Thr Ala Ser Leu Gln Asn Phe Asn Ile Ser Asn Leu Gln
2355 2360 2365

Lys Ser Ile Ser Asn Pro Pro Gly Ser Asn Leu Arg Thr Thr
2370 2375 2380

<210> 41
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: S_TKc,
Serine/Threonine protein kinases domain sequence

<400> 41
Val Leu Gly Lys Gly Ala Phe Gly Lys Val Tyr Leu Ala Arg Asp Lys
1 5 10 15
Lys Thr Gly Lys Leu Val Ala Ile Lys Val Ile Lys Lys Glu Lys Leu
20 25 30
Lys Lys Lys Arg Glu Arg Ile Leu Arg Glu Ile Lys Ile Leu Lys
35 40 45
Lys Leu Asp His Pro Asn Ile Val Lys Leu Tyr Asp Val Phe Glu Asp
50 55 60
Asp Asp Lys Leu Tyr Leu Val Met Glu Tyr Cys Glu Gly Gly Asp Leu
65 70 75 80
Phe Asp Leu Leu Lys Lys Arg Gly Arg Leu Ser Glu Asp Glu Ala Arg
85 90 95
Phe Tyr Ala Arg Gln Ile Leu Ser Ala Leu Glu Tyr Leu His Ser Gln
100 105 110
Gly Ile Ile His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Ser
115 120 125
Asp Gly His Val Lys Leu Ala Asp Phe Gly Leu Ala Lys Gln Leu Asp
130 135 140
Ser Gly Gly Thr Leu Leu Thr Thr Phe Val Gly Thr Pro Glu Tyr Met
145 150 155 160
Ala Pro Glu Val Leu Leu Gly Lys Gly Tyr Gly Lys Ala Val Asp Ile
165 170 175
Trp Ser Leu Gly Val Ile Leu Tyr Glu Leu Leu Thr Gly Lys Pro Pro
180 185 190
Phe Pro Gly Asp Asp Gln Leu Leu Ala Leu Phe Lys Lys Ile Gly Lys

195	200	205
Pro Pro Pro Pro Phe Pro Pro Pro Glu Trp Lys Ile Ser Pro Glu Ala		
210	215	220
Lys Asp Leu Ile Lys Lys Leu Leu Val Lys Asp Pro Glu Lys Arg Leu		
225	230	235
Thr Ala Glu Glu Ala Leu Glu His Pro Phe Phe		
245	250	
<210> 42		
<211> 251		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: pkinase,		
Protein kinase domain sequence		
<400> 42		
Lys Leu Gly Ser Gly Ala Phe Gly Lys Val Tyr Lys Gly Lys His Lys		
1	5	10
15		
Asp Thr Gly Glu Ile Val Ala Ile Lys Ile Leu Lys Lys Arg Ser Leu		
20	25	30
Ser Glu Lys Lys Lys Arg Phe Leu Arg Glu Ile Gln Ile Leu Arg Arg		
35	40	45
Leu Ser His Pro Asn Ile Val Arg Leu Leu Gly Val Phe Glu Glu Asp		
50	55	60
Asp His Leu Tyr Leu Val Met Glu Tyr Met Glu Gly Gly Asp Leu Phe		
65	70	75
80		
Asp Tyr Leu Arg Arg Asn Gly Leu Leu Leu Ser Glu Lys Glu Ala Lys		
85	90	95
Lys Ile Ala Leu Gln Ile Leu Arg Gly Leu Glu Tyr Leu His Ser Arg		
100	105	110
Gly Ile Val His Arg Asp Leu Lys Pro Glu Asn Ile Leu Leu Asp Glu		
115	120	125
Asn Gly Thr Val Lys Ile Ala Asp Phe Gly Leu Ala Arg Lys Leu Glu		
130	135	140

Ser	Ser	Ser	Tyr	Glu	Lys	Leu	Thr	Thr	Phe	Val	Gly	Thr	Pro	Glu	Tyr
145						150				155				160	
Met	Ala	Pro	Glu	Val	Leu	Glu	Gly	Arg	Gly	Tyr	Ser	Ser	Lys	Val	Asp
						165			170					175	
Val	Trp	Ser	Leu	Gly	Val	Ile	Leu	Tyr	Glu	Leu	Leu	Thr	Gly	Lys	Leu
						180			185				190		
Pro	Phe	Pro	Gly	Ile	Asp	Pro	Leu	Glu	Glu	Leu	Phe	Arg	Ile	Lys	Glu
	195					200					205				
Arg	Pro	Arg	Leu	Arg	Leu	Pro	Leu	Pro	Pro	Asn	Cys	Ser	Glu	Glu	Leu
	210					215					220				
Lys	Asp	Leu	Ile	Lys	Lys	Cys	Leu	Asn	Lys	Asp	Pro	Glu	Lys	Arg	Pro
	225				230					235			240		
Thr	Ala	Lys	Glu	Ile	Leu	Asn	His	Pro	Trp	Phe					
					245			250							

<210> 43
 <211> 254
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: TyrKc,
 Tyrosine kinase domain sequence

<400> 43
 Leu Thr Leu Gly Lys Lys Leu Gly Glu Gly Ala Phe Gly Glu Val Tyr
 1 5 10 15

Lys Gly Thr Leu Lys Gly Lys Gly Val Glu Val Glu Val Ala Val
 20 25 30

Lys Thr Leu Lys Glu Asp Ala Ser Glu Gln Gln Ile Glu Glu Phe Leu
 35 40 45

Arg Glu Ala Arg Leu Met Arg Lys Leu Asp His Pro Asn Ile Val Lys
 50 55 60

Leu Leu Gly Val Cys Thr Glu Glu Glu Pro Leu Met Ile Val Met Glu
 65 70 75 80

Tyr	Met	Glu	Gly	Gly	Asp	Leu	Leu	Asp	Tyr	Leu	Arg	Lys	Asn	Arg	Pro
						85				90					95
Lys	Glu	Leu	Ser	Leu	Ser	Asp	Leu	Leu	Ser	Phe	Ala	Leu	Gln	Ile	Ala
						100			105						110
Arg	Gly	Met	Glu	Tyr	Leu	Glu	Ser	Lys	Asn	Phe	Val	His	Arg	Asp	Leu
						115			120						125
Ala	Ala	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Lys	Thr	Val	Lys	Ile	Ala
						130			135						140
Asp	Phe	Gly	Leu	Ala	Arg	Asp	Leu	Tyr	Asp	Asp	Tyr	Tyr	Arg	Lys	
						145			150			155			160
Lys	Lys	Ser	Pro	Arg	Leu	Pro	Ile	Arg	Trp	Met	Ala	Pro	Glu	Ser	Leu
						165			170						175
Lys	Asp	Gly	Lys	Phe	Thr	Ser	Lys	Ser	Asp	Val	Trp	Ser	Phe	Gly	Val
						180			185						190
Leu	Leu	Trp	Glu	Ile	Phe	Thr	Leu	Gly	Glu	Ser	Pro	Tyr	Pro	Gly	Met
						195			200			205			
Ser	Asn	Glu	Glu	Val	Leu	Glu	Tyr	Leu	Lys	Lys	Gly	Tyr	Arg	Leu	Pro
						210			215			220			
Gln	Pro	Pro	Asn	Cys	Pro	Asp	Glu	Ile	Tyr	Asp	Leu	Met	Leu	Gln	Cys
						225			230			235			240
Trp	Ala	Glu	Asp	Pro	Glu	Asp	Arg	Pro	Thr	Phe	Ser	Glu	Leu		
						245			250						

<210> 44
 <211> 314
 <212> PRT
 <213> Homo sapiens

<400> 44															
Met	Asp	Gly	Thr	Asn	Gly	Ser	Thr	Gln	Thr	His	Phe	Ile	Leu	Leu	Gly
1				5					10					15	
Phe	Ser	Asp	Arg	Pro	His	Leu	Glu	Arg	Ile	Leu	Phe	Val	Val	Ile	Leu
						20			25					30	
Ile	Ala	Tyr	Leu	Leu	Thr	Leu	Val	Gly	Asn	Thr	Thr	Ile	Ile	Leu	Val
						35			40					45	

Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60

His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro Gln
 65 70 75 80

Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met Gly
 85 90 95

Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Val Glu Cys
 100 105 110

Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys Lys
 115 120 125

Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly Leu
 130 135 140

Val Ser Val Thr Trp Gly Cys Gly Val Ala Asn Ser Leu Ala Met Ser
 145 150 155 160

Pro Val Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp His
 165 170 175

Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser Thr
 180 185 190

Val Ala Ile Glu Gly Thr Val Phe Val Leu Lys Lys Gly Val Val Leu
 195 200 205

Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg Ala
 210 215 220

Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly Thr
 225 230 235 240

Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile
 245 250 255

Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly Met
 260 265 270

Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro Leu
 275 280 285

Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg Leu
 290 295 300

Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu
305 310

<210> 45
<211> 233
<212> PRT
<213> Marmota marmota

<400> 45
Pro Met Tyr Leu Phe Leu Gly Asn Leu Ser Phe Leu Asp Leu Ser Phe
1 5 10 15

Thr Ser Ser Ile Pro Gln Leu Leu His Asn Leu Ser Gly Arg Asp Lys
20 25 30

Thr Ile Ser Tyr Val Gly Cys Val Val Gln Leu Phe Leu Phe Leu Gly
35 40 45

Leu Gly Gly Val Glu Cys Leu Leu Leu Ala Val Ala Tyr Asp Arg Val
50 55 60

Ala Val Cys Lys Pro Leu His Tyr Thr Val Ile Met Ser Ser Arg Leu
65 70 75 80

Cys Leu Gly Leu Val Ser Val Ala Trp Gly Cys Gly Met Ala Asn Ser
85 90 95

Leu Val Met Ser Pro Val Thr Leu Gln Leu Pro Arg Cys Gly His Asn
100 105 110

Lys Val Asp His Phe Leu Cys Glu Met Pro Ala Ile Arg Met Ala Cys
115 120 125

Val Asn Thr Val Ala Ile Glu Gly Thr Val Phe Val Leu Ala Val Gly
130 135 140

Ile Val Leu Ser Pro Leu Val Phe Ile Leu Val Ser Tyr Gly His Ile
145 150 155 160

Val Arg Ala Val Phe Arg Ile Gln Ser Ser Ser Gly Arg His Arg Ile
165 170 175

Phe Asn Thr Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly
180 185 190

Asn Ile Ile Tyr Met Tyr Met Gln Pro Gly Ser Arg Ser Ser Gln Asp

195	200	205
Gln Gly Lys Phe Leu Thr Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu		
210	215	220
Asn Pro Phe Ile Tyr Ser Leu Arg Asn		
225	230	
<210> 46		
<211> 320		
<212> PRT		
<213> Homo sapiens		
<400> 46		
Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly		
1	5	10
		15
Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala		
20	25	30
Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala		
35	40	45
Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg		
50	55	60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln		
65	70	75
		80
Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly		
85	90	95
Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys		
100	105	110
Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys		
115	120	125
Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met		
130	135	140
Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys		
145	150	155
		160
Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His		
165	170	175

Phe	Leu	Cys	Glu	Leu	Pro	Ala	Leu	Val	Lys	Ile	Ala	Cys	Val	Asp	Thr
180															190
Thr	Thr	Val	Glu	Met	Ser	Val	Phe	Ala	Leu	Gly	Ile	Ile	Ile	Val	Leu
195															205
Thr	Pro	Leu	Ile	Leu	Ile	Leu	Ile	Ser	Tyr	Gly	Ile	Ala	Lys	Ala	
210															220
Val	Leu	Arg	Thr	Lys	Ser	Lys	Ala	Ser	Gln	Arg	Lys	Ala	Met	Asn	Thr
225															240
Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ser	Met	Phe	Tyr	Gly	Thr	Ile	Ile
245															255
Tyr	Met	Tyr	Leu	Gln	Pro	Gly	Asn	Arg	Ala	Ser	Lys	Asp	Gln	Gly	Lys
260															270
Phe	Leu	Thr	Leu	Phe	Tyr	Thr	Val	Ile	Thr	Pro	Ser	Leu	Asn	Pro	Leu
275															285
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Met	Lys	Asp	Ala	Leu	Lys	Lys	Leu
290															300
Met	Arg	Phe	His	His	Lys	Ser	Thr	Lys	Ile	Lys	Arg	Asn	Cys	Lys	Ser
305															320

<210> 47
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 47															
Met	Asp	Gln	Ser	Asn	Tyr	Ser	Ser	Leu	His	Gly	Phe	Ile	Leu	Leu	Gly
1															15
Phe	Ser	Asn	His	Pro	Lys	Met	Glu	Met	Ile	Leu	Ser	Gly	Val	Val	Ala
20															30
Ile	Phe	Tyr	Leu	Ile	Thr	Leu	Val	Gly	Asn	Thr	Ala	Ile	Ile	Leu	Ala
35															45
Ser	Leu	Leu	Asp	Ser	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Arg
50															60

Asn	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Thr	Ser	Ile	Ile	Pro	Gln
65				70					75					80	
Val	Leu	Val	Asn	Leu	Trp	Gly	Pro	Asp	Lys	Thr	Ile	Ser	Tyr	Val	Gly
				85					90					95	
Cys	Ile	Ile	Gln	Leu	Tyr	Val	Tyr	Met	Trp	Leu	Gly	Ser	Val	Glu	Cys
					100			105					110		
Leu	Leu	Leu	Ala	Val	Met	Ser	Tyr	Asp	Arg	Phe	Thr	Ala	Ile	Cys	Lys
					115			120					125		
Pro	Leu	His	Tyr	Phe	Val	Val	Met	Asn	Pro	His	Leu	Cys	Leu	Lys	Met
					130			135					140		
Ile	Ile	Met	Ile	Trp	Ser	Ile	Ser	Leu	Ala	Asn	Ser	Val	Val	Leu	Cys
					145			150					155		160
Thr	Leu	Thr	Leu	Asn	Leu	Pro	Thr	Cys	Gly	Asn	Asn	Ile	Leu	Asp	His
					165				170				175		
Phe	Leu	Cys	Glu	Leu	Pro	Ala	Leu	Val	Lys	Ile	Ala	Cys	Val	Asp	Thr
					180				185				190		
Thr	Thr	Val	Glu	Met	Ser	Val	Phe	Ala	Leu	Gly	Ile	Ile	Ile	Val	Leu
					195			200					205		
Thr	Pro	Leu	Ile	Leu	Ile	Leu	Ile	Ser	Tyr	Gly	Tyr	Ile	Ala	Lys	Ala
					210			215					220		
Val	Leu	Arg	Thr	Lys	Ser	Lys	Ala	Ser	Gln	Arg	Lys	Ala	Met	Asn	Thr
					225			230					235		240
Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ser	Met	Phe	Tyr	Gly	Thr	Ile	Ile
					245				250				255		
Tyr	Met	Tyr	Leu	Gln	Pro	Gly	Asn	Arg	Ala	Ser	Lys	Asp	Gln	Gly	Lys
					260				265				270		
Phe	Leu	Thr	Leu	Phe	Tyr	Thr	Val	Ile	Thr	Pro	Ser	Leu	Asn	Pro	Leu
					275			280					285		
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Met	Lys	Asp	Ala	Leu	Lys	Lys	Leu
					290			295					300		
Met	Arg	Phe	His	His	Lys	Ser	Thr	Lys	Ile	Lys	Arg	Asn	Cys	Lys	Ser
					305			310					315		320

<210> 48

<211> 320

<212> PRT

<213> Homo sapiens

<400> 48

Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly

1

5

10

15

Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala

20

25

30

Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala

35

40

45

Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg

50

55

60

Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln

65

70

75

80

Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly

85

90

95

Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys

100

105

110

Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys

115

120

125

Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met

130

135

140

Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys

145

150

155

160

Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His

165

170

175

Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr

180

185

190

Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu

195

200

205

Thr Pro Leu Ile Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala
210 215 220

Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr
225 230 235 240

Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile
245 250 255

Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys
260 265 270

Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu
275 280 285

Ile Tyr Thr Leu Arg Asn Lys Asn Met Lys Asp Ala Leu Lys Lys Leu
290 295 300

Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys Lys Ser
305 310 315 320

<210> 49

<211> 253

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 7tm_1, 7
transmembrane receptor domain sequence

<400> 49

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg
1 5 10 15

Thr Pro Thr Asn Ile Phe Leu Leu Asn Leu Ala Val Ala Asp Leu Leu
20 25 30

Phe Leu Leu Thr Leu Pro Pro Trp Ala Leu Tyr Tyr Leu Val Gly Gly
35 40 45

Asp Trp Val Phe Gly Asp Ala Leu Cys Lys Leu Gly Ala Leu Phe Val
50 55 60

Val Asn Gly Tyr Ala Ser Ile Leu Leu Leu Thr Ala Ile Ser Ile Asp			
65	70	75	80
Arg Tyr Leu Ala Ile Val His Pro Leu Arg Tyr Arg Arg Ile Arg Thr			
85	90	95	
Pro Arg Arg Ala Lys Val Leu Ile Leu Leu Val Trp Val Leu Ala Leu			
100	105	110	
Leu Leu Ser Leu Pro Pro Leu Leu Phe Ser Trp Leu Arg Thr Val Glu			
115	120	125	
Glu Gly Asn Thr Thr Val Cys Leu Ile Asp Phe Pro Glu Glu Ser Val			
130	135	140	
Lys Arg Ser Tyr Val Leu Leu Ser Thr Leu Val Gly Phe Val Leu Pro			
145	150	155	160
Leu Leu Val Ile Leu Val Cys Tyr Thr Arg Ile Leu Arg Thr Leu Arg			
165	170	175	
Lys Arg Ala Arg Ser Gln Arg Ser Leu Lys Arg Arg Ser Ser Ser Glu			
180	185	190	
Arg Lys Ala Ala Lys Met Leu Leu Val Val Val Val Phe Val Leu			
195	200	205	
Cys Trp Leu Pro Tyr His Ile Val Leu Leu Leu Asp Ser Leu Cys Leu			
210	215	220	
Leu Ser Ile Trp Arg Val Leu Pro Thr Ala Leu Leu Ile Thr Leu Trp			
225	230	235	240
Leu Ala Tyr Val Asn Ser Cys Leu Asn Pro Ile Ile Tyr			
245	250		
<210> 50			
<211> 315			
<212> PRT			
<213> Homo sapiens			
<400> 50			
Met Ala Gln Leu Gly Gly Ala Ala Asn Arg Ala Pro Thr Ala Ser Leu			
1	5	10	15
Ala Pro Thr Ser Gln Ser Leu Arg Cys Ala Pro Gln Pro Arg Pro Ser			

20	25	30
Arg Ala Asp Thr Gly Ser Leu Gly Arg Tyr Trp Gly Lys Ala Ala Ala		
35	40	45
Ala Ala Ser Arg Glu His Pro Phe Pro Gly Thr Leu Met His Ser Ala		
50	55	60
Ala Gly Ser Gly Arg Arg Arg Gly Ala Leu Arg Glu Leu Leu Gly Leu		
65	70	75
Gln Arg Ala Ala Pro Ala Gly Trp Leu Ser Glu Glu Arg Ala Glu Glu		
85	90	95
Leu Gly Gly Pro Ser Gly Pro Gly Ser Ser Arg Leu Cys Leu Glu Pro		
100	105	110
Arg Glu His Ala Trp Ile Leu Ala Ala Ala Glu Gly Arg Tyr Glu Val		
115	120	125
Leu Arg Glu Leu Leu Glu Ala Glu Pro Glu Leu Leu Arg Gly Asp		
130	135	140
Pro Ile Thr Gly Tyr Ser Val Leu His Trp Leu Ala Lys His Gly Arg		
145	150	155
His Glu Glu Leu Ile Leu Val His Asp Phe Ala Leu Arg Arg Gly Leu		
165	170	175
Arg Leu Asp Val Ser Ala Pro Gly Ser Gly Gly Leu Thr Pro Leu His		
180	185	190
Leu Ala Ala Leu Gln Gly His Asp Met Val Ile Lys Val Leu Val Gly		
195	200	205
Ala Leu Gly Ala Asp Ala Thr Arg Arg Asp His Ser Gly His Arg Ala		
210	215	220
Cys His Tyr Leu Arg Pro Asp Ala Pro Trp Arg Leu Arg Glu Leu Ser		
225	230	235
Gly Ala Glu Glu Trp Glu Met Glu Ser Gly Ser Gly Cys Thr Asn Leu		
245	250	255
Asn Asn Asn Ser Ser Gly Thr Thr Ala Trp Arg Ala Ala Ser Ala Val		
260	265	270
Gly Ala Thr Ala Val Glu Thr Ser Arg Arg Val Ala Ala Ser Arg Thr		

275 280 285
Lys Ala Lys Asp Thr Ala Gly Ser Arg Val Ala Gln Met His Ser Leu
290 295 300

Phe Arg His Leu Phe Pro Ser Phe Gln Asp Arg
305 310 315

<210> 51
<211> 32
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: domain
sequence

<400> 51
Gly Asn Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Glu Val
1 5 10 15

Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Val Asn Ala Arg Asp Lys
20 25 30

<210> 52
<211> 2062
<212> PRT
<213> Homo sapiens

<400> 52
Met Pro Lys Ser Gly Phe Thr Lys Pro Ile Gln Ser Glu Asn Ser Asp
1 5 10 15

Ser Asp Ser Asn Met Val Glu Lys Pro Tyr Gly Arg Lys Ser Lys Asp
20 25 30

Lys Ile Ala Ser Tyr Ser Lys Thr Pro Lys Ile Glu Arg Ser Asp Val
35 40 45

Ser Lys Glu Met Lys Glu Lys Ser Ser Met Lys Arg Lys Leu Pro Phe
50 55 60

Thr Ile Ser Pro Ser Arg Asn Glu Glu Arg Asp Ser Asp Thr Asp Ser

65	70	75	80
Asp Pro Gly His Thr Ser Glu Asn Trp Gly Glu Arg Leu Ile Ser Ser			
85	90	95	
Tyr Arg Thr Tyr Ser Glu Lys Glu Gly Pro Glu Lys Lys Lys Thr Lys			
100	105	110	
Lys Glu Ala Gly Asn Lys Lys Ser Thr Pro Val Ser Ile Leu Phe Gly			
115	120	125	
Tyr Pro Leu Ser Glu Arg Lys Gln Met Ala Leu Leu Met Gln Met Thr			
130	135	140	
Ala Arg Asp Asn Ser Pro Asp Ser Thr Pro Asn His Pro Ser Gln Thr			
145	150	155	160
Thr Pro Ala Gln Lys Lys Thr Pro Ser Ser Ser Arg Gln Lys Asp			
165	170	175	
Lys Val Asn Lys Arg Asn Glu Arg Gly Glu Thr Pro Leu His Met Ala			
180	185	190	
Ala Ile Arg Gly Asp Val Lys Gln Val Lys Glu Leu Ile Ser Leu Gly			
195	200	205	
Ala Asn Val Asn Val Lys Asp Phe Ala Gly Trp Thr Pro Leu His Glu			
210	215	220	
Ala Cys Asn Val Gly Tyr Tyr Asp Val Ala Lys Ile Leu Ile Ala Ala			
225	230	235	240
Gly Ala Asp Val Asn Thr Gln Gly Leu Asp Asp Asp Thr Pro Leu His			
245	250	255	
Asp Ser Ala Ser Ser Gly His Arg Asp Ile Val Lys Leu Leu Leu Arg			
260	265	270	
His Gly Gly Asn Pro Phe Gln Ala Asn Lys His Gly Glu Arg Pro Val			
275	280	285	
Asp Val Ala Glu Thr Glu Glu Leu Glu Leu Leu Lys Arg Glu Val			
290	295	300	
Pro Leu Ser Asp Asp Asp Glu Ser Tyr Thr Asp Ser Glu Glu Ala Gln			
305	310	315	320
Ser Val Asn Pro Ser Ser Val Asp Glu Asn Ile Asp Ser Glu Thr Glu			

325	330	335
Lys Asp Ser Leu Ile Cys Glu Ser Lys Gln Ile Leu Pro Ser Lys Thr		
340	345	350
Pro Leu Pro Ser Ala Leu Asp Glu Tyr Glu Phe Lys Asp Asp Asp Asp		
355	360	365
Glu Glu Ile Asn Lys Met Ile Asp Asp Arg His Ile Leu Arg Lys Glu		
370	375	380
Gln Arg Lys Glu Asn Glu Pro Glu Ala Glu Lys Thr His Leu Phe Ala		
385	390	395
Lys Gln Glu Lys Ala Phe Tyr Pro Lys Ser Phe Lys Ser Lys Lys Gln		
405	410	415
Lys Pro Ser Arg Val Leu Tyr Ser Ser Thr Glu Ser Ser Asp Glu Glu		
420	425	430
Ala Leu Gln Asn Lys Lys Ile Ser Thr Ser Cys Ser Val Ile Pro Glu		
435	440	445
Thr Ser Asn Ser Asp Met Gln Thr Lys Lys Glu Tyr Val Val Ser Gly		
450	455	460
Glu His Lys Gln Lys Gly Lys Val Lys Arg Lys Leu Lys Asn Gln Asn		
465	470	475
Lys Asn Lys Glu Asn Gln Glu Leu Lys Gln Glu Lys Glu Gly Lys Glu		
485	490	495
Asn Thr Arg Ile Thr Asn Leu Thr Val Asn Thr Gly Leu Asp Cys Ser		
500	505	510
Glu Lys Thr Arg Glu Glu Gly Asn Phe Arg Lys Ser Phe Ser Pro Lys		
515	520	525
Asp Asp Thr Ser Leu His Leu Phe His Ile Ser Thr Gly Lys Ser Pro		
530	535	540
Lys His Ser Cys Gly Leu Ser Glu Lys Gln Ser Thr Pro Leu Lys Gln		
545	550	555
Glu His Thr Lys Thr Cys Leu Ser Pro Gly Ser Ser Glu Met Ser Leu		
565	570	575
Gln Pro Asp Leu Val Arg Tyr Asp Asn Thr Glu Ser Glu Phe Leu Pro		

580 585 590
Glu Ser Ser Ser Val Lys Ser Cys Lys His Lys Glu Lys Ser Lys His
595 600 605
Gln Lys Asp Phe His Leu Glu Phe Gly Glu Lys Ser Asn Ala Lys Ile
610 615 620
Lys Asp Glu Asp His Ser Pro Thr Phe Glu Asn Ser Asp Cys Thr Leu
625 630 635 640
Lys Lys Met Asp Lys Glu Gly Lys Thr Leu Lys Lys His Lys Leu Lys
645 650 655
His Lys Glu Arg Glu Lys Glu Lys His Lys Lys Glu Ile Glu Gly Glu
660 665 670
Lys Glu Lys Tyr Lys Thr Lys Asp Ser Ala Lys Glu Leu Gln Arg Ser
675 680 685
Val Glu Phe Asp Arg Glu Phe Trp Lys Glu Asn Phe Phe Lys Ser Asp
690 695 700
Glu Thr Glu Asp Leu Phe Leu Asn Met Glu His Glu Ser Leu Thr Leu
705 710 715 720
Glu Lys Lys Ser Lys Leu Glu Lys Asn Ile Lys Asp Asp Lys Ser Thr
725 730 735
Lys Glu Lys His Val Ser Lys Glu Arg Asn Phe Lys Glu Glu Arg Asp
740 745 750
Lys Ile Lys Lys Glu Ser Glu Lys Ser Phe Arg Glu Glu Lys Ile Lys
755 760 765
Asp Leu Lys Glu Glu Arg Glu Asn Ile Pro Thr Asp Lys Asp Ser Glu
770 775 780
Phe Thr Ser Leu Gly Met Ser Ala Ile Glu Glu Ser Ile Gly Leu His
785 790 795 800
Leu Val Glu Lys Glu Ile Asp Ile Glu Lys Gln Glu Lys His Ile Lys
805 810 815
Glu Ser Lys Glu Lys Pro Glu Lys Arg Ser Gln Ile Lys Glu Lys Asp
820 825 830
Ile Glu Lys Met Glu Arg Lys Thr Phe Glu Lys Glu Lys Lys Ile Lys

835 840 845
His Glu His Lys Ser Glu Lys Asp Lys Leu Asp Leu Ser Glu Cys Val
850 855 860
Asp Lys Ile Lys Glu Lys Asp Lys Leu Tyr Ser His His Thr Glu Lys
865 870 875 880
Cys His Lys Glu Gly Glu Lys Ser Lys Asn Thr Ala Ala Ile Lys Lys
885 890 895
Thr Asp Asp Arg Glu Lys Ser Arg Glu Lys Met Asp Arg Lys His Asp
900 905 910
Lys Glu Lys Pro Glu Lys Glu Arg His Leu Ala Glu Ser Lys Glu Lys
915 920 925
His Leu Met Glu Lys Lys Asn Lys Gln Ser Asp Asn Ser Glu Tyr Ser
930 935 940
Lys Ser Glu Lys Gly Lys Asn Lys Glu Lys Asp Arg Glu Leu Asp Lys
945 950 955 960
Lys Glu Lys Ser Arg Asp Lys Glu Ser Ile Asn Ile Thr Asn Ser Lys
965 970 975
His Ile Gln Glu Glu Lys Lys Ser Ser Ile Val Asp Gly Asn Lys Ala
980 985 990
Gln His Glu Lys Pro Leu Ser Leu Lys Glu Lys Thr Lys Asp Glu Pro
995 1000 1005
Leu Lys Thr Pro Asp Gly Lys Glu Lys Asp Lys Lys Asp Lys Asp Ile
1010 1015 1020
Asp Arg Tyr Lys Glu Arg Asp Lys His Lys Asp Lys Ile Gln Ile Asn
1025 1030 1035 1040
Ser Leu Leu Lys Leu Lys Ser Glu Ala Asp Lys Pro Lys Pro Lys Ser
1045 1050 1055
Ser Pro Ala Ser Lys Asp Thr Arg Pro Lys Glu Lys Arg Leu Val Asn
1060 1065 1070
Asp Asp Leu Met Gln Thr Ser Phe Glu Arg Met Leu Ser Leu Lys Asp
1075 1080 1085
Leu Glu Ile Glu Gln Trp His Lys Lys His Lys Glu Lys Ile Lys Gln

1090 1095 1100
Lys Glu Lys Glu Arg Leu Arg Asn Arg Asn Cys Leu Glu Leu Lys Ile
1105 1110 1115 1120
Lys Asp Lys Glu Lys Thr Lys His Thr Pro Thr Glu Ser Lys Asn Lys
1125 1130 1135
Glu Leu Thr Arg Ser Lys Ser Ser Glu Val Thr Asp Ala Tyr Thr Lys
1140 1145 1150
Glu Lys Gln Pro Lys Asp Ala Val Ser Asn Arg Ser Gln Ser Val Asp
1155 1160 1165
Thr Lys Asn Val Met Thr Leu Gly Lys Ser Ser Phe Val Ser Asp Asn
1170 1175 1180
Ser Leu Asn Arg Ser Pro Arg Ser Glu Asn Glu Lys Pro Gly Leu Ser
1185 1190 1195 1200
Ser Arg Ser Val Ser Met Ile Ser Val Ala Ser Ser Glu Asp Ser Cys
1205 1210 1215
His Thr Thr Val Thr Pro Arg Pro Pro Val Glu Tyr Asp Ser Asp
1220 1225 1230
Phe Met Leu Glu Ser Ser Glu Ser Gln Met Ser Phe Ser Gln Ser Pro
1235 1240 1245
Phe Leu Ser Ile Ala Lys Ser Pro Ala Leu His Glu Arg Glu Leu Asp
1250 1255 1260
Ser Leu Ala Asp Leu Pro Glu Arg Ile Lys Pro Pro Tyr Ala Asn Arg
1265 1270 1275 1280
Leu Ser Thr Ser His Leu Arg Ser Ser Ser Val Glu Asp Val Lys Leu
1285 1290 1295
Ile Ile Ser Glu Gly Arg Pro Thr Ile Glu Val Arg Arg Cys Ser Met
1300 1305 1310
Pro Ser Val Ile Cys Glu His Thr Lys Gln Phe Gln Thr Ile Ser Glu
1315 1320 1325
Glu Ser Asn Gln Gly Ser Leu Leu Thr Val Pro Gly Asp Thr Ser Pro
1330 1335 1340
Ser Pro Lys Pro Glu Val Phe Ser Asn Val Pro Glu Arg Asp Leu Ser

1345	1350	1355	1360
Asn Val Ser Asn Ile His Ser Ser Phe Ala Thr Ser Pro Thr Gly Ala			
1365	1370	1375	
Ser Asn Ser Lys Tyr Val Ser Ala Asp Arg Asn Leu Ile Lys Asn Thr			
1380	1385	1390	
Ala Pro Val Asn Thr Val Met Asp Ser Pro Val His Leu Glu Pro Ser			
1395	1400	1405	
Ser Gln Val Gly Val Ile Gln Asn Lys Ser Trp Glu Met Pro Val Asp			
1410	1415	1420	
Arg Leu Glu Thr Leu Ser Thr Arg Asp Phe Ile Cys Pro Asn Ser Asn			
1425	1430	1435	1440
Ile Pro Asp Gln Glu Ser Ser Leu Gln Ser Phe Cys Asn Ser Glu Asn			
1445	1450	1455	
Lys Val Leu Lys Glu Asn Ala Asp Phe Leu Ser Leu Arg Gln Thr Glu			
1460	1465	1470	
Leu Pro Gly Asn Ser Cys Ala Gln Asp Pro Ala Ser Phe Met Pro Pro			
1475	1480	1485	
Gln Gln Pro Cys Ser Phe Pro Ser Gln Ser Leu Ser Asp Ala Glu Ser			
1490	1495	1500	
Ile Ser Lys His Met Ser Leu Ser Tyr Val Ala Asn Gln Glu Pro Gly			
1505	1510	1515	1520
Ile Leu Gln Gln Lys Asn Ala Val Gln Ile Ile Ser Ser Ala Leu Asp			
1525	1530	1535	
Thr Asp Asn Glu Ser Thr Lys Asp Thr Glu Asn Thr Phe Val Leu Gly			
1540	1545	1550	
Asp Val Gln Lys Thr Asp Ala Phe Val Pro Val Tyr Ser Asp Ser Thr			
1555	1560	1565	
Ile Gln Glu Ala Ser Pro Asn Phe Glu Lys Ala Tyr Thr Leu Pro Val			
1570	1575	1580	
Leu Pro Ser Glu Lys Asp Phe Asn Gly Ser Asp Ala Ser Thr Gln Leu			
1585	1590	1595	1600
Asn Thr His Tyr Ala Phe Ser Lys Leu Thr Tyr Lys Ser Ser Ser Gly			

1605	1610	1615
His Glu Val Glu Asn Ser Thr Thr Asp Thr Gln Val Ile Ser His Glu		
1620	1625	1630
Lys Glu Asn Lys Leu Glu Ser Leu Val Leu Thr His Leu Ser Arg Cys		
1635	1640	1645
Asp Ser Asp Leu Cys Glu Met Asn Ala Gly Met Pro Lys Gly Asn Leu		
1650	1655	1660
Asn Glu Gln Asp Pro Lys His Cys Pro Glu Ser Glu Lys Cys Leu Leu		
1665	1670	1675
Ser Ile Glu Asp Glu Glu Ser Gln Gln Ser Ile Leu Ser Ser Leu Glu		
1685	1690	1695
Asn His Ser Gln Gln Ser Thr Gln Pro Glu Met His Lys Tyr Gly Gln		
1700	1705	1710
Leu Val Lys Val Glu Leu Glu Asn Ala Glu Asp Asp Lys Thr Glu		
1715	1720	1725
Asn Gln Ile Pro Gln Arg Met Thr Arg Asn Lys Ala Asn Thr Met Ala		
1730	1735	1740
Asn Gln Ser Lys Gln Ile Leu Ala Ser Cys Thr Leu Leu Ser Glu Lys		
1745	1750	1755
Asp Ser Glu Ser Ser Ser Pro Arg Gly Arg Ile Arg Leu Thr Glu Asp		
1765	1770	1775
Asp Asp Pro Gln Ile His His Pro Arg Lys Arg Lys Val Ser Arg Val		
1780	1785	1790
Pro Gln Pro Val Gln Val Ser Pro Ser Leu Leu Gln Ala Lys Glu Lys		
1795	1800	1805
Thr Gln Gln Ser Leu Ala Ala Ile Val Asp Ser Leu Lys Leu Asp Glu		
1810	1815	1820
Ile Gln Pro Tyr Ser Ser Glu Arg Ala Asn Pro Tyr Phe Glu Tyr Leu		
1825	1830	1835
His Ile Arg Lys Lys Ile Glu Glu Lys Arg Lys Leu Leu Cys Ser Val		
1845	1850	1855
Ile Pro Gln Ala Pro Gln Tyr Tyr Asp Glu Tyr Val Thr Phe Asn Gly		

1860	1865	1870
Ser Tyr Leu Leu Asp Gly Asn Pro Leu Ser Lys Ile Cys Ile Pro Thr		
1875	1880	1885
Ile Thr Pro Pro Pro Ser Leu Ser Asp Pro Leu Lys Glu Leu Phe Arg		
1890	1895	1900
Gln Gln Glu Val Val Arg Met Lys Leu Arg Leu Gln His Ser Ile Glu		
1905	1910	1915
1920		
Arg Glu Lys Leu Ile Val Ser Asn Glu Gln Glu Val Leu Arg Val His		
1925	1930	1935
Tyr Arg Ala Ala Arg Thr Leu Ala Asn Gln Thr Leu Pro Phe Ser Ala		
1940	1945	1950
Cys Thr Val Leu Leu Asp Ala Glu Val Tyr Asn Val Pro Leu Asp Ser		
1955	1960	1965
Gln Ser Asp Asp Ser Lys Thr Ser Val Arg Asp Arg Phe Asn Ala Arg		
1970	1975	1980
Gln Phe Met Ser Trp Leu Gln Asp Val Asp Asp Lys Phe Asp Lys Leu		
1985	1990	1995
2000		
Lys Thr Cys Leu Leu Met Arg Gln Gln His Glu Ala Ala Ala Leu Asn		
2005	2010	2015
Ala Val Gln Arg Leu Glu Trp Gln Leu Lys Leu Gln Glu Leu Asp Pro		
2020	2025	2030
Ala Thr Tyr Lys Ser Ile Ser Ile Tyr Glu Ile Gln Glu Phe Tyr Val		
2035	2040	2045
Pro Leu Val Asp Val Asn Asp Asp Phe Glu Leu Thr Pro Ile		
2050	2055	2060
<210> 53		
<211> 399		
<212> PRT		
<213> Homo sapiens		
<400> 53		
Met Pro Gln Ser Ser Ala Lys Asp Tyr Leu Gly Glu Tyr Cys Ile Leu		
1	5	10
15		

Lys Ala Gln Ala Ala Asp Gly Ala Gly Pro Glu Asp Asp Thr Glu Ala
20 25 30

Ser Arg Ala Ala Ala Pro Ala Glu Gly Pro Pro Gly Gly Ile Gln Pro
35 40 45

Glu Ala Ala Glu Pro Lys Pro Thr Ala Glu Ala Pro Lys Ala Pro Arg
50 55 60

Val Glu Glu Ile Pro Gln Arg Met Thr Arg Asn Arg Ala Gln Met Leu
65 70 75 80

Ala Asn Gln Ser Lys Gln Gly Pro Pro Pro Ser Glu Lys Glu Cys Ala
85 90 95

Pro Thr Pro Ala Pro Val Thr Arg Ala Lys Ala Arg Gly Ser Glu Asp
100 105 110

Asp Asp Ala Gln Ala Gln His Pro Arg Lys Arg Arg Phe Gln Arg Ser
115 120 125

Thr Gln Gln Leu Gln Gln Leu Asn Thr Ser Thr Gln Gln Thr Arg
130 135 140

Glu Val Ile Gln Gln Thr Leu Ala Ala Ile Val Asp Ala Ile Lys Leu
145 150 155 160

Asp Ala Ile Glu Pro Tyr His Ser Asp Arg Ala Asn Pro Tyr Phe Glu
165 170 175

Tyr Leu Gln Ile Arg Lys Lys Ile Glu Glu Lys Arg Lys Ile Leu Cys
180 185 190

Cys Ile Thr Pro Gln Ala Pro Gln Trp Tyr Ala Gln Tyr Val Thr Tyr
195 200 205

Thr Gly Ser Tyr Leu Leu Asp Gly Lys Pro Leu Ser Lys Leu His Ile
210 215 220

Pro Val Ile Ala Pro Pro Pro Ser Leu Ala Glu Pro Leu Lys Glu Leu
225 230 235 240

Phe Arg Gln Gln Glu Ala Val Arg Gly Lys Leu Arg Leu Gln His Ser
245 250 255

Ile Glu Arg Glu Lys Leu Ile Val Ser Cys Glu Gln Glu Ile Leu Arg
260 265 270

Val His Cys Arg Ala Ala Arg Thr Ile Ala Asn Gln Ala Val Pro Phe
275 280 285

Ser Thr Cys Thr Met Leu Leu Asp Ser Glu Val Tyr Asn Met Pro Leu
290 295 300

Glu Ser Gln Gly Asp Glu Asn Lys Ser Val Arg Asp Arg Phe Asn Ala
305 310 315 320

Arg Gln Phe Ile Ser Trp Leu Gln Asp Val Asp Asp Lys Tyr Asp Arg
325 330 335

Met Lys Thr Cys Leu Leu Met Arg Gln Gln His Glu Ala Ala Ala Leu
340 345 350

Asn Ala Val Gln Arg Met Glu Trp Gln Leu Lys Val Gln Glu Leu Asp
355 360 365

Pro Ala Gly His Lys Ser Leu Cys Val Asn Glu Val Pro Ser Phe Tyr
370 375 380

Val Pro Met Val Asp Val Asn Asp Asp Phe Val Leu Leu Pro Ala
385 390 395

<210> 54

<211> 366

<212> PRT

<213> Homo sapiens

<400> 54

Met Pro Lys Gly Gly Cys Pro Lys Ala Pro Gln Gln Glu Leu Pro
1 5 10 15

Leu Ser Ser Asp Met Val Glu Lys Gln Thr Gly Lys Lys Asp Lys Asp
20 25 30

Lys Val Ser Leu Thr Lys Thr Pro Lys Leu Glu Arg Gly Asp Gly Gly
35 40 45

Lys Glu Val Arg Glu Arg Ala Ser Lys Arg Lys Leu Pro Phe Thr Ala
50 55 60

Gly Ala Asn Gly Glu Gln Lys Asp Ser Asp Thr Glu Lys Gln Gly Pro
65 70 75 80

Glu Arg Lys Arg Ile Lys Lys Glu Pro Val Thr Arg Lys Ala Gly Leu
85 90 95

Leu Phe Gly Met Gly Leu Ser Gly Ile Arg Ala Gly Tyr Pro Leu Ser
100 105 110

Glu Arg Gln Gln Val Ala Leu Leu Met Gln Met Thr Ala Glu Glu Ser
115 120 125

Ala Asn Ser Pro Val Asp Thr Thr Pro Lys His Pro Ser Gln Ser Thr
130 135 140

Val Cys Gln Lys Gly Thr Pro Asn Ser Ala Ser Lys Thr Lys Asp Lys
145 150 155 160

Leu Asn Lys Arg Asn Glu Arg Gly Glu Thr Arg Leu His Arg Ala Ala
165 170 175

Ile Arg Gly Asp Ala Arg Arg Ile Lys Glu Leu Ile Ser Glu Gly Ala
180 185 190

Asp Val Asn Val Lys Asp Phe Ala Gly Trp Thr Ala Leu His Glu Ala
195 200 205

Cys Asn Arg Gly Tyr Tyr Asp Val Ala Lys Gln Leu Leu Ala Ala Gly
210 215 220

Ala Glu Val Asn Thr Lys Gly Leu Asp Asp Asp Thr Pro Leu His Asp
225 230 235 240

Ala Ala Asn Asn Gly His Tyr Lys Val Val Lys Leu Leu Leu Arg Tyr
245 250 255

Gly Gly Asn Pro Gln Gln Ser Asn Arg Lys Gly Glu Thr Pro Leu Lys
260 265 270

Val Ala Asn Ser Pro Thr Met Val Asn Leu Leu Leu Gly Lys Gly Thr
275 280 285

Tyr Thr Ser Ser Glu Glu Ser Ser Thr Glu Ser Ser Glu Glu Glu Asp
290 295 300

Ala Pro Ser Phe Ala Pro Ser Ser Ser Val Asp Gly Asn Asn Thr Asp
305 310 315 320

Ser Glu Phe Glu Lys Gly Ser Ser Thr Arg Pro Arg Thr Gln Ser His
325 330 335

Arg Arg Pro Arg Pro Pro Ser Arg Thr Ser Met Ser Leu Met Arg Thr
340 345 350

Thr Ser Arg Thr Gly Phe Leu Arg Trp Thr Thr Ser Thr Tyr
355 360 365

<210> 55
<211> 366
<212> PRT
<213> Homo sapiens

<400> 55
Met Pro Lys Gly Gly Cys Pro Lys Ala Pro Gln Gln Glu Glu Leu Pro
1 5 10 15
Leu Ser Ser Asp Met Val Glu Lys Gln Thr Gly Lys Lys Asp Lys Asp
20 25 30
Lys Val Ser Leu Thr Lys Thr Pro Lys Leu Glu Arg Gly Asp Gly Gly
35 40 45
Lys Glu Val Arg Glu Arg Ala Ser Lys Arg Lys Leu Pro Phe Thr Ala
50 55 60
Gly Ala Asn Gly Glu Gln Lys Asp Ser Asp Thr Glu Lys Gln Gly Pro
65 70 75 80
Glu Arg Lys Arg Ile Lys Lys Glu Pro Val Thr Arg Lys Ala Gly Leu
85 90 95
Leu Phe Gly Met Gly Leu Ser Gly Ile Arg Ala Gly Tyr Pro Leu Ser
100 105 110
Glu Arg Gln Gln Val Ala Leu Leu Met Gln Met Thr Ala Glu Glu Ser
115 120 125
Ala Asn Ser Pro Val Asp Thr Thr Pro Lys His Pro Ser Gln Ser Thr
130 135 140
Val Cys Gln Lys Gly Thr Pro Asn Ser Ala Ser Lys Thr Lys Asp Lys
145 150 155 160
Leu Asn Lys Arg Asn Glu Arg Gly Glu Thr Arg Leu His Arg Ala Ala
165 170 175
Ile Arg Gly Asp Ala Arg Arg Ile Lys Glu Leu Ile Ser Glu Gly Ala
180 185 190
Asp Val Asn Val Lys Asp Phe Ala Gly Trp Thr Ala Leu His Glu Ala

195	200	205
Cys Asn Arg Gly Tyr Tyr Asp Val Ala Lys Gln Leu Leu Ala Ala Gly		
210	215	220
Ala Glu Val Asn Thr Lys Gly Leu Asp Asp Asp Thr Pro Leu His Asp		
225	230	235
Ala Ala Asn Asn Gly His Tyr Lys Val Val Lys Leu Leu Leu Arg Tyr		
245	250	255
Gly Gly Asn Pro Gln Gln Ser Asn Arg Lys Gly Glu Thr Pro Leu Lys		
260	265	270
Val Ala Asn Ser Pro Thr Met Val Asn Leu Leu Leu Gly Lys Gly Thr		
275	280	285
Tyr Thr Ser Ser Glu Glu Ser Ser Thr Glu Ser Ser Glu Glu Glu Asp		
290	295	300
Ala Pro Ser Phe Ala Pro Ser Ser Ser Val Asp Gly Asn Asn Thr Asp		
305	310	315
320		
Ser Glu Phe Glu Lys Gly Ser Ser Thr Arg Pro Arg Thr Gln Ser His		
325	330	335
Arg Arg Pro Arg Pro Pro Ser Arg Thr Ser Met Ser Leu Met Arg Thr		
340	345	350
Thr Ser Arg Thr Gly Phe Leu Arg Trp Thr Thr Ser Thr Tyr		
355	360	365
<210> 56		
<211> 601		
<212> PRT		
<213> Homo sapiens		
<400> 56		
Asn Ala Asp Phe Leu Ser Leu Arg Gln Thr Glu Leu Pro Gly Asn Ser		
1	5	10
15		
Cys Ala Gln Asp Pro Ala Ser Phe Met Pro Pro Gln Gln Pro Cys Ser		
20	25	30
Phe Pro Ser Gln Ser Leu Ser Asp Ala Glu Ser Ile Ser Lys His Met		
35	40	45

Ser Leu Ser Tyr Val Ala Asn Gln Glu Pro Gly Ile Leu Gln Gln Lys
 50 55 60

Asn Ala Val Gln Ile Ile Ser Ser Ala Leu Asp Thr Asp Asn Glu Ser
 65 70 75 80

Thr Lys Asp Thr Glu Asn Thr Phe Val Leu Gly Asp Val Gln Lys Thr
 85 90 95

Asp Ala Phe Val Pro Val Tyr Ser Asp Ser Thr Ile Gln Glu Ala Ser
 100 105 110

Pro Asn Phe Glu Lys Ala Tyr Thr Leu Pro Val Leu Pro Ser Glu Lys
 115 120 125

Asp Phe Asn Gly Ser Asp Ala Ser Thr Gln Leu Asn Thr His Tyr Ala
 130 135 140

Phe Ser Lys Leu Thr Tyr Lys Ser Ser Ser Gly His Glu Val Glu Asn
 145 150 155 160

Ser Thr Thr Asp Thr Gln Val Ile Ser His Glu Lys Glu Asn Lys Leu
 165 170 175

Glu Ser Leu Val Leu Thr His Leu Ser Arg Cys Asp Ser Asp Leu Cys
 180 185 190

Glu Met Asn Ala Gly Met Pro Lys Gly Asn Leu Asn Glu Gln Asp Pro
 195 200 205

Lys His Cys Pro Glu Ser Glu Lys Cys Leu Leu Ser Ile Glu Asp Glu
 210 215 220

Glu Ser Gln Gln Ser Ile Leu Ser Ser Leu Glu Asn His Ser Gln Gln
 225 230 235 240

Ser Thr Gln Pro Glu Met His Lys Tyr Gly Gln Leu Val Lys Val Glu
 245 250 255

Leu Glu Glu Asn Ala Glu Asp Asp Lys Thr Glu Asn Gln Ile Pro Gln
 260 265 270

Arg Met Thr Arg Asn Lys Ala Asn Thr Met Ala Asn Gln Ser Lys Gln
 275 280 285

Ile Leu Ala Ser Cys Thr Leu Leu Ser Glu Lys Asp Ser Glu Ser Ser
 290 295 300

Ser Pro Arg Gly Arg Ile Arg Leu Thr Glu Asp Asp Asp Pro Gln Ile
 305 310 315 320

His His Pro Arg Lys Arg Lys Val Ser Arg Val Pro Gln Pro Val Gln
 325 330 335

Val Ser Pro Ser Leu Leu Gln Ala Lys Glu Lys Thr Gln Gln Ser Leu
 340 345 350

Ala Ala Ile Val Asp Ser Leu Lys Leu Asp Glu Ile Gln Pro Tyr Ser
 355 360 365

Ser Glu Arg Ala Asn Pro Tyr Phe Glu Tyr Leu His Ile Arg Lys Lys
 370 375 380

Ile Glu Glu Lys Arg Lys Leu Leu Cys Ser Val Ile Pro Gln Ala Pro
 385 390 395 400

Gln Tyr Tyr Asp Glu Tyr Val Thr Phe Asn Gly Ser Tyr Leu Leu Asp
 405 410 415

Gly Asn Pro Leu Ser Lys Ile Cys Ile Pro Thr Ile Thr Pro Pro Pro
 420 425 430

Ser Leu Ser Asp Pro Leu Lys Glu Leu Phe Arg Gln Gln Glu Val Val
 435 440 445

Arg Met Lys Leu Arg Leu Gln His Ser Ile Glu Arg Glu Lys Leu Ile
 450 455 460

Val Ser Asn Glu Gln Glu Val Leu Arg Val His Tyr Arg Ala Ala Arg
 465 470 475 480

Thr Leu Ala Asn Gln Thr Leu Pro Phe Ser Ala Cys Thr Val Leu Leu
 485 490 495

Asp Ala Glu Val Tyr Asn Val Pro Leu Asp Ser Gln Ser Asp Asp Ser
 500 505 510

Lys Thr Ser Val Arg Asp Arg Phe Asn Ala Arg Gln Phe Met Ser Trp
 515 520 525

Leu Gln Asp Val Asp Asp Lys Phe Asp Lys Leu Lys Thr Cys Leu Leu
 530 535 540

Met Arg Gln Gln His Glu Ala Ala Ala Leu Asn Ala Val Gln Arg Leu
 545 550 555 560

Glu Trp Gln Leu Lys Leu Gln Glu Leu Asp Pro Ala Thr Tyr Lys Ser
565 570 575

Ile Ser Ile Tyr Glu Ile Gln Glu Phe Tyr Val Pro Leu Val Asp Val
580 585 590

Asn Asp Asp Phe Glu Leu Thr Pro Ile
595 600

<210> 57

<211> 999

<212> PRT

<213> Homo sapiens

<400> 57

Met Ile Ser Glu Glu Lys Glu Trp Leu Phe Lys Asp Glu Ile Ile Lys
1 5 10 . 15

Val Ser Lys Asp Glu Lys Ser Leu Lys Arg Ile Lys Gly Met Asn Lys
20 25 30

Asp Ile Ser Arg Ser Phe Gln Glu Glu Lys Asp Cys Ser Asn Thr Ala
35 40 45

Glu Lys Glu Lys Ser Leu Lys Glu Lys Ser Ser Lys Glu Glu Lys Leu
50 55 60

Arg Leu Tyr Lys Glu Glu Arg Lys Thr Pro Lys Arg Gln Lys Asp Lys
65 70 75 80

Glu Pro Lys Asp Lys Arg Lys Asp Thr Gly Ala Ala Asp Gly Val Thr
85 90 95

Asp Lys Lys Glu Lys Val Leu Glu Lys His Lys Glu Lys Lys Val Lys
100 105 110

Glu Tyr Gln Lys Asn Lys Lys Asn Lys Gln Lys Leu Pro Glu Lys Ala
115 120 125

Glu Lys Lys Gln Ser Ala Glu Asp Lys Ala Asn Ser Lys His Lys Glu
130 135 140

Lys Ser Asp Lys Glu Tyr Ser Lys Glu Arg Lys Ser Leu Arg Ser Ala
145 150 155 160

Asp Met Glu Lys Ser Leu Leu Glu Lys Leu Glu Glu Ala Leu His Glu
165 170 175

Tyr Arg Asp Asp Ser Ser Asp Lys Ile Thr Thr Thr Glu Arg Asp Ser
180 185 190

Gln Glu Arg Lys Val Pro Glu Glu Lys Gly Arg Asp Tyr Lys Glu Gly
195 200 205

Gly Ser Arg Lys Asp Thr Gly Gln Tyr Glu Lys Asp Phe Leu Glu Met
210 215 220

Val Ala Tyr Gly Val Ser Tyr Asn Met Lys Ala Val Ile Glu Asp Arg
225 230 235 240

Leu Asn Lys Thr Val Glu Leu Phe Ser Thr Glu Lys Lys Asp Lys Asn
245 250 255

Asp Ser Glu Arg Glu Thr Ser Lys Lys Ile Glu Lys Glu Leu Lys Pro
260 265 270

Tyr Gly Ser Arg Thr Lys Gln Lys Pro Thr Ala Arg Asp Lys Asp Ser
275 280 285

Pro Pro Arg Ala Leu Lys Asp Lys Ser Arg Asp Glu Asp Pro Arg Leu
290 295 300

Arg Lys Ala Lys Leu Lys Glu Lys Phe Lys Asp Ser Ala Glu Lys Glu
305 310 315 320

Lys Asp Asp Ser Val Lys Met Ser Lys Gly Asp Asp Lys Val Ser Pro
325 330 335

Ser Lys Asp Pro Gly Lys Lys Asn Ala Arg Pro Arg Glu Lys Leu Arg
340 345 350

Gly Asp Gly Asp Met Met Ile Ile Ser Phe Gln Arg Met Phe Ser Gln
355 360 365

Lys Asp Leu Glu Ile Glu Glu Arg His Lys Gly His Lys Glu Arg Met
370 375 380

Lys Gln Met Glu Lys Leu Arg His Gln Ser Arg Asp Pro Asn Leu Lys
385 390 395 400

Glu Arg Ala Lys Pro Ala Asp Asp Gly Arg Lys Lys Gly Leu Glu Ile
405 410 415

Pro Ala Lys Lys Pro Pro Gly Leu Asp Pro Pro Phe Lys Asp Lys Lys
420 425 430

Leu Lys Glu Leu Thr Pro Ile Pro Pro Ala Ala Glu Asn Lys Pro Arg
435 440 445

Pro Gly Ser Gly Ala Asp Ser Lys Asp Trp Leu Ala Gly Pro His Met
450 455 460

Lys Glu Val Leu Pro Ala Ser Pro Arg Pro Asp Gln Ser Arg Pro Val
465 470 475 480

Cys Pro Pro Leu Arg Arg Cys Cys Pro Ala Ser Ala Thr Arg Arg Gly
485 490 495

His Ser Pro Ala Pro Gly Arg His Arg Gly Pro Ala Gly Tyr Ser Pro
500 505 510

His His Pro Pro Gly Ala Gln Leu Pro Gly Ala Ala Gly Arg Gly Leu
515 520 525

Ile Gly Ser Ala Ser Glu Asn Pro Val Ser Trp Pro Val Gly Ser Glu
530 535 540

Leu Leu Leu Lys Ser Pro Gln Arg Phe Pro Glu Ser Pro Glu Tyr Phe
545 550 555 560

Cys Ser Ala Asp Ser Leu His Ser Ala Ala Pro Gly Pro Phe Ser Ala
565 570 575

Ser Glu Asn Thr Leu Leu Ile Ala Glu Pro Gly Leu Glu Asp Val Lys
580 585 590

Asp Arg Val Glu Ala Ile Pro Ala Thr Ile Ser Thr Ser Glu Ala Ala
595 600 605

Pro Tyr Ala Pro Pro Ser Gly Leu Glu Ser Phe Phe Asn Asn Cys Lys
610 615 620

Ser Leu Pro Glu Ser Leu Leu Asp Met Ala Pro Glu Ala Cys Asn His
625 630 635 640

Cys Gly Ser Asp Ala Phe Ala Gly Ser Glu Asp Asp Leu Asp Leu Gly
645 650 655

Ser Phe Ser Leu Pro Glu Leu Pro Leu Gln Thr Lys Asp Val Pro Asp
660 665 670

Val Glu Thr Glu Pro Thr Glu Glu Ser Leu Ala Pro Ser Glu Lys Ile
675 680 685

Pro Pro Gly Ala Pro Val Val Leu Pro Thr Glu Leu Glu Pro Glu Pro
690 695 700

Ser Glu Glu Pro Lys Leu Asp Val Ala Leu Glu Ala Thr Glu Ala Glu
705 710 715 720

Ala Val Pro Glu Glu Arg Ala Ser Gly Asp Leu Asp Ser Ser Met Glu
725 730 735

Pro Thr Pro Val Arg Pro Glu Gln Cys Gln Leu Gly Ser Arg Asp Gln
740 745 750

Gly Ala Glu Ala Glu His Leu Leu Pro Pro Ala Ala Ser Leu Cys Ala
755 760 765

Pro Asp Thr Pro Cys Pro Pro Trp Thr Leu Trp His Lys Pro Arg Leu
770 775 780

Arg Thr Val Leu Ala Pro Thr Thr Leu Arg Ala Ser Arg Ala Ala
785 790 795 800

Ala Pro Ala Glu Gly Pro Pro Cys Gly Ile Asp Pro Glu Ala Thr Glu
805 810 815

Ser Glu Pro Lys Pro Thr Ala Glu Ala Pro Lys Ala Pro Arg His Ser
820 825 830

Thr Gln Gln Leu Asn Thr Ser Thr Gln Gln Thr Arg Glu Val Ile Gln
835 840 845

Gln Thr Leu Ala Thr Ile Val Asp Ala Ile Lys Leu Asp Ala Ile Tyr
850 855 860

Pro Tyr His Ser Asp Arg Ala Asn Pro Tyr Phe Glu Phe Leu His Ile
865 870 875 880

Arg Lys Lys Ile Glu Glu Lys Arg Lys Ile Leu Cys Cys Ile Thr Pro
885 890 895

Gln Ala Thr Gln Trp Tyr Ala Glu Tyr Val Thr Tyr Thr Gly Ser Tyr
900 905 910

Leu Leu Asp Gly Lys Ser Leu Ser Lys Leu His Met Pro Met Ile Ala
915 920 925

Pro Pro Pro Ser Leu Arg Ala Ser Ala Thr Arg Thr Ser Gln Cys Ala
930 935 940

Thr Gly Ser Thr Pro Ala Ser Ser Ser Pro Gly Ser Met Thr Trp Thr
945 950 955 960

Thr Ile Gln Pro His Glu Asp Leu Leu Thr Trp Gln Gln His Glu Ala
965 970 975

Ala Ala Leu Asn Ala Met Gln Arg Met Glu Trp Gln Leu Lys Val Gln
980 985 990

Lys Leu Asp Pro Ala Gly His
995

<210> 58
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ANK, ankyrin
repeats domain sequence

<400> 58
Gly Asn Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Glu Val
1 5 10 15

Val Lys Leu Leu Glu Ala Gly Ala Asp Val Asn
20 25

<210> 59
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ANK, ankyrin
repeats domain sequence

<400> 59
Asp Gly Asn Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Glu
1 5 10 15

Val Val Lys Leu Leu Glu Ala Gly Ala Asp Val Asn Ala Arg Asp
20 25 30

Lys

<210> 60
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ANK, ankyrin
repeats domain sequence

<400> 60
Gly Asn Thr Pro Leu His Leu Ala Ala Arg Asn Gly His Leu Glu Val
1 5 10 15

Val Lys Leu Leu Leu Glu Ala Gly Ala Asp Val Asn Ala Arg Asp
20 25 30

<210> 61
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ANK, ankyrin
repeats domain sequence

<400> 61
Gly Arg Thr Pro Leu His Leu Ala Ala Glu Asn Gly Asn Leu Glu Val
1 . 5 10 15

Val Lys Leu Leu Leu Asp Lys Gly Ala Asp Ile Asn
20 25

<210> 62
<211> 28
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ANK, ankyrin
repeats domain sequence

<400> 62
Asp Gly Arg Thr Pro Leu His Leu Ala Ala Glu Asn Gly Asn Leu Glu

1

5

10

15

Val Val Lys Leu Leu Leu Asp Lys Gly Ala Asp Ile
20 25

<210> 63
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ANK, ankyrin
repeats domain sequence

<400> 63
Gly Arg Thr Pro Leu His Leu Ala Ala Glu Asn Gly Asn Leu Glu Val
1 5 10 15

Val Lys Leu Leu Leu Asp Lys Gly Ala Asp Ile Asn Leu
20 25

<210> 64
<211> 287
<212> PRT
<213> Homo sapiens

<400> 64
Met Pro Pro Thr Lys Pro Phe Leu Ala Pro Glu Thr Thr Ser Pro Gly
1 5 10 15

Asp Arg Val Glu Thr Pro Val Gly Glu Arg Ala Pro Thr Pro Val Ser
20 25 30

Ala Ser Ser Glu Val Ser Pro Glu Ser Gln Glu Asp Ser Glu Thr Pro
35 40 45

Ala Glu Glu Asp Ser Gly Ser Glu Gln Pro Pro Asn Ser Val Leu Pro
50 55 60

Asp Lys Leu Lys Val Ser Trp Glu Asn Pro Ser Pro Gln Glu Ala Pro
65 70 75 80

Ala Ala Glu Ser Ala Glu Ser Ser Gln Ala Pro Cys Ser Glu Thr Ser
85 90 95

Glu Ala Ala Pro Arg Glu Gly Gly Lys Pro Pro Thr Pro Pro Pro Lys

100	105	110
Ile Leu Ser Glu Lys Leu Lys Ala Ser Met Gly Glu Met Gln Ala Ser		
115	120	125
Gly Pro Pro Ala Pro Gly Thr Val Gln Val Ser Val Asn Gly Met Asp		
130	135	140
Asp Ser Pro Glu Pro Ala Lys Pro Ser Gln Ala Glu Gly Thr Pro Gly		
145	150	155
160		
Thr Pro Pro Lys Asp Ala Thr Thr Ser Thr Ala Leu Pro Pro Trp Asp		
165	170	175
Leu Pro Pro Gln Phe His Pro Arg Cys Ser Ser Leu Gly Asp Leu Leu		
180	185	190
Gly Glu Gly Pro Arg His Pro Leu Gln Pro Arg Glu Arg Leu Tyr Arg		
195	200	205
Ala Gln Leu Glu Val Lys Val Ala Ser Glu Gln Thr Glu Lys Leu Leu		
210	215	220
Asn Lys Val Leu Gly Ser Glu Pro Ala Pro Val Ser Ala Glu Thr Leu		
225	230	235
240		
Leu Ser Gln Ala Val Glu Gln Leu Arg Gln Ala Thr Gln Val Leu Gln		
245	250	255
Glu Met Arg Asp Leu Gly Glu Leu Ser Gln Glu Ala Pro Gly Leu Arg		
260	265	270
Glu Lys Arg Lys Glu Leu Val Thr Leu Tyr Arg Arg Ser Ala Pro		
275	280	285
<210> 65		
<211> 99		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence: Pleckstrin		
homology domain sequence		
<400> 65		
Ile Val Lys Glu Gly Trp Leu Leu Lys Lys Ser Thr Val Lys Lys Lys		
1	5	10
		15

Arg Trp Lys Lys Arg Tyr Phe Phe Leu Phe Asn Asp Val Leu Ile Tyr
20 25 30

Tyr Lys Asp Lys Lys Ser Tyr Glu Pro Lys Gly Ser Ile Pro Leu
35 40 45

Ser Gly Cys Ser Val Glu Asp Val Pro Asp Ser Glu Phe Lys Arg Pro
50 55 60

Asn Cys Phe Gln Leu Arg Ser Arg Asp Gly Lys Glu Thr Phe Ile Leu
65 70 75 80

Gln Ala Glu Ser Glu Glu Arg Gln Asp Trp Ile Lys Ala Ile Gln
85 90 95

Ser Ala Ile

<210> 66

<211> 103

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Pleckstrin
homology domain sequence

<400> 66

Val Ile Lys Glu Gly Trp Leu Leu Lys Lys Ser Ser Gly Gly Lys Lys
1 5 10 15

Ser Trp Lys Lys Arg Tyr Phe Val Leu Phe Asn Gly Val Leu Leu Tyr
20 25 30

Tyr Lys Ser Lys Lys Lys Ser Ser Ser Lys Pro Lys Gly Ser Ile
35 40 45

Pro Leu Ser Gly Cys Thr Val Arg Glu Ala Pro Asp Ser Asp Ser Asp
50 55 60

Lys Lys Lys Asn Cys Phe Glu Ile Val Thr Pro Asp Arg Lys Thr Leu
65 70 75 80

Leu Leu Gln Ala Glu Ser Glu Glu Arg Lys Glu Trp Val Glu Ala
85 90 95

Leu Arg Lys Ala Ile Ala Lys

100

<210> 67

<211> 431

<212> PRT

<213> Mus musculus

<400> 67

Met Arg Arg Leu Arg Arg Leu Val His Leu Val Leu Leu Cys Pro Phe
1 5 10 15

Ser Lys Gly Leu Gln Gly Arg Leu Pro Gly Leu Arg Val Lys Tyr Val
20 25 30

Leu Leu Val Trp Leu Gly Ile Phe Val Gly Ser Trp Met Val Tyr Val
35 40 45

His Tyr Ser Ser Tyr Ser Glu Leu Cys Arg Gly His Val Cys Gln Val
50 55 60

Val Ile Cys Asp Gln Tyr Arg Lys Gly Ile Ile Ser Gly Ser Val Cys
65 70 75 80

Gln Asp Leu Cys Glu Leu Gln Lys Val Glu Trp Arg Thr Cys Leu Ser
85 90 95

Ser Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp Gln Asp Lys Glu
100 105 110

Val Thr Ile Lys Cys Gly Ile Glu Glu Ala Leu Asn Ser Lys Ala Trp
115 120 125

Pro Asp Ala Ala Pro Arg Arg Glu Leu Val Leu Phe Asp Lys Pro Thr
130 135 140

Arg Gly Thr Ser Ile Lys Glu Phe Arg Glu Met Thr Leu Ser Phe Leu
145 150 155 160

Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala Leu Val Asp Gln
165 170 175

Ile Leu Leu Met Ala Asp Phe Asn Lys Asp Ser Arg Val Ser Leu Ala
180 185 190

Glu Ala Lys Ser Val Trp Ala Leu Leu Gln Arg Asn Glu Phe Leu Leu
195 200 205

Leu Leu Ser Leu Gln Glu Lys Glu His Ala Ser Arg Leu Leu Gly Tyr
 210 215 220

 Cys Gly Asp Leu Tyr Leu Thr Glu Gly Ile Pro His Gly Ser Trp His
 225 230 235 240

 Gly Ala Val Leu Leu Pro Ala Leu Arg Pro Leu Leu Pro Ser Val Leu
 245 250 255

 His Arg Ala Leu Gln Gln Trp Phe Gly Pro Ala Trp Pro Trp Arg Ala
 260 265 270

 Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu Glu Leu Phe His Gly
 275 280 285

 Ser Tyr Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu Ala Asn Val Gly
 290 295 300

 Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu Gln Gln Val Ala
 305 310 315 320

 Pro Glu Ala Thr Val Arg Arg Phe Leu Gln Gly Arg His Cys Glu Gln
 325 330 335

 Ser Ser Asp Cys Ile Tyr Gly Arg Asp Cys Arg Ala Pro Cys Asp Arg
 340 345 350

 Leu Met Arg Gln Cys Lys Gly Asp Leu Ile Gln Pro Asn Leu Ala Lys
 355 360 365

 Val Cys Glu Leu Leu Arg Asp Tyr Leu Leu Pro Gly Ala Pro Ala Gly
 370 375 380

 Leu Tyr Glu Glu Leu Gly Lys Gln Leu Arg Thr Cys Thr Thr Leu Ser
 385 390 395 400

 Gly Leu Ala Ser Gln Ile Glu Ala His His Ser Leu Val Leu Ser His
 405 410 415

 Leu Lys Thr Leu Leu Trp Arg Glu Ile Ser Asn Thr Asn Tyr Ser
 420 425 430

<210> 68
 <211> 428
 <212> PRT
 <213> Mus musculus

<400> 68

Met Val Tyr Val His Tyr Ser Ser Tyr Ser Glu Leu Cys Arg Gly His
1 5 10 15

Val Cys Gln Val Val Ile Cys Asp Gln Tyr Arg Lys Gly Ile Ile Ser
20 25 30

Gly Ser Val Cys Gln Asp Leu Cys Glu Leu Gln Lys Val Glu Trp Arg
35 40 45

Thr Cys Leu Ser Ser Ala Pro Gly Gln Gln Val Tyr Ser Gly Leu Trp
50 55 60

Gln Asp Lys Glu Val Thr Ile Lys Cys Gly Ile Glu Glu Ala Leu Asn
65 70 75 80

Ser Lys Ala Trp Pro Asp Ala Ala Pro Arg Arg Glu Leu Val Leu Phe
85 90 95

Asp Lys Pro Thr Arg Gly Thr Ser Ile Lys Glu Phe Arg Glu Met Thr
100 105 110

Leu Ser Phe Leu Lys Ala Asn Leu Gly Asp Leu Pro Ser Leu Pro Ala
115 120 125

Leu Val Asp Gln Ile Leu Leu Met Ala Asp Phe Asn Lys Asp Ser Arg
130 135 140

Val Ser Leu Ala Glu Ala Lys Ser Val Trp Ala Leu Leu Gln Arg Asn
145 150 155 160

Glu Phe Leu Leu Leu Ser Leu Gln Glu Lys Glu His Ala Ser Arg
165 170 175

Leu Leu Gly Tyr Cys Gly Asp Leu Tyr Leu Thr Glu Gly Ile Pro His
180 185 190

Gly Ser Trp His Gly Ala Val Leu Leu Pro Ala Leu Arg Pro Leu Leu
195 200 205

Pro Ser Val Leu His Arg Ala Leu Gln Gln Trp Phe Gly Pro Ala Trp
210 215 220

Pro Trp Arg Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu Glu
225 230 235 240

Leu Phe His Gly Ser Tyr Gly Thr Phe Tyr Met Cys Glu Thr Thr Leu

245	250	255
Ala Asn Val Gly Tyr Thr Ala Thr Tyr Asp Phe Lys Met Ala Asp Leu		
260	265	270
Gln Gln Val Ala Pro Glu Ala Thr Val Arg Arg Phe Leu Gln Gly Arg		
275	280	285
His Cys Glu Gln Ser Ser Asp Cys Ile Tyr Gly Arg Asp Cys Arg Ala		
290	295	300
Pro Cys Asp Arg Leu Met Arg Gln Cys Lys Gly Asp Leu Ile Gln Pro		
305	310	315
Asn Leu Ala Lys Val Cys Glu Leu Leu Arg Asp Tyr Leu Leu Pro Gly		
325	330	335
Ala Pro Ala Gly Leu Tyr Glu Glu Leu Gly Lys Gln Cys Ala Pro Ala		
340	345	350
Pro Gln Lys Val Asp Trp Pro Ala Arg Leu Arg Leu Thr Ile His Trp		
355	360	365
Cys Leu Ala Thr Leu Arg Pro Tyr Ser Gly Gly Arg Ser Pro Thr Pro		
370	375	380
Thr Thr Pro Arg Ala Ala Gly Ser Arg His Tyr Ser Ser Gln Val Ala		
385	390	395
Pro Pro His Ser Leu Gln Gln Leu Ser Arg Gly Ala Arg Gly Pro Tyr		
405	410	415
Gln Arg Trp Pro Thr Gly Pro Asn Pro Pro Asn Met		
420	425	

<210> 69
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 69
 Met Val Glu Trp Arg Thr Cys Leu Ser Val Ala Pro Gly Gln Gln Val
 1 5 10 15
 Tyr Ser Gly Leu Trp Arg Asp Lys Asp Val Thr Ile Lys Cys Gly Ile
 20 25 30

Glu	Glu	Thr	Leu	Asp	Ser	Lys	Ala	Arg	Ser	Asp	Ala	Ala	Pro	Arg	Arg
35							40						45		
Glu	Leu	Val	Leu	Phe	Asp	Lys	Pro	Thr	Arg	Gly	Thr	Ser	Ile	Lys	Glu
50							55						60		
Phe	Arg	Glu	Met	Thr	Leu	Gly	Phe	Leu	Lys	Ala	Asn	Leu	Gly	Asp	Leu
65							70						75		80
Pro	Ser	Leu	Pro	Ala	Leu	Val	Gly	Gln	Val	Leu	Leu	Met	Ala	Asp	Phe
									85			90		95	
Asn	Lys	Asp	Asn	Arg	Val	Ser	Leu	Ala	Glu	Ala	Lys	Ser	Val	Trp	Ala
									100			105		110	
Leu	Leu	Gln	Arg	Asn	Glu	Phe	Leu	Leu	Leu	Ser	Leu	Gln	Glu	Lys	
							115					120		125	
Glu	His	Ala	Ser	Arg	Leu	Leu	Gly	Tyr	Cys	Gly	Asp	Leu	Tyr	Leu	Thr
							130					135		140	
Glu	Gly	Val	Pro	His	Gly	Ala	Trp	His	Ala	Ala	Ala	Leu	Pro	Pro	Leu
145							150					155		160	
Leu	Arg	Pro	Leu	Leu	Pro	Pro	Ala	Leu	Gln	Gly	Ala	Leu	Gln	Gln	Trp
							165					170		175	
Leu	Gly	Pro	Ala	Trp	Pro	Trp	Arg	Ala	Lys	Ile	Ala	Ile	Gly	Leu	Leu
							180					185		190	
Glu	Phe	Val	Glu	Glu	Leu	Phe	His	Gly	Ser	Tyr	Gly	Thr	Phe	Tyr	Met
							195					200		205	
Cys	Glu	Thr	Thr	Leu	Ala	Asn	Val	Gly	Tyr	Thr	Ala	Thr	Tyr	Asp	Phe
							210					215		220	
Lys	Met	Ala	Asp	Leu	Gln	Gln	Val	Ala	Pro	Glu	Ala	Thr	Val	Arg	Arg
225							230					235		240	
Phe	Leu	Gln	Gly	Arg	Arg	Cys	Glu	His	Ser	Thr	Asp	Cys	Thr	Thr	Gly
							245					250		255	
Ala	Thr	Ala	Gly	Pro	Arg	Val	Thr	Gly	Ser						
							260					265			

<210> 70

<211> 428

<212> PRT

<213> Mus musculus

<400> 70

Met Ala Arg Ser Leu Cys Ala Gly Ala Trp Leu Arg Lys Pro His Tyr
1 5 10 15

Leu Gln Ala Arg Leu Ser Tyr Met Arg Val Lys Tyr Leu Phe Phe Ser
20 25 30

Trp Leu Val Val Phe Val Gly Ser Trp Ile Ile Tyr Val Gln Tyr Ser
35 40 45

Thr Tyr Thr Glu Leu Cys Arg Gly Lys Asp Cys Lys Lys Ile Ile Cys
50 55 60

Asp Lys Tyr Lys Thr Gly Val Ile Asp Gly Pro Ala Cys Asn Ser Leu
65 70 75 80

Cys Val Thr Glu Thr Leu Tyr Phe Gly Lys Cys Leu Ser Asn Lys Pro
85 90 95

Ser Asn Gln Met Tyr Leu Gly Val Trp Asp Asn Leu Pro Gly Val Val
100 105 110

Lys Cys Gln Met Glu Gln Ala Leu His Leu Asp Phe Gly Thr Glu Leu
115 120 125

Glu Pro Arg Lys Glu Ile Val Leu Phe Asp Lys Pro Thr Arg Gly Thr
130 135 140

Thr Val Gln Lys Phe Lys Glu Met Val Tyr Ser Leu Phe Lys Ala Lys
145 150 155 160

Leu Gly Asp Gln Gly Asn Leu Ser Glu Leu Val Asn Leu Ile Leu Thr
165 170 175

Val Ala Asp Gly Asp Arg Asp Gly Gln Val Ser Leu Gly Glu Ala Lys
180 185 190

Ser Ala Trp Ala Leu Leu Gln Leu Asn Glu Phe Leu Leu Met Val Ile
195 200 205

Leu Gln Asp Lys Glu His Thr Pro Lys Leu Met Gly Phe Cys Gly Asp
210 215 220

Leu Tyr Val Met Glu Ser Val Glu Tyr Thr Ser Leu Tyr Gly Ile Ser
225 230 235 240

Leu	Pro	Trp	Val	Met	Glu	Leu	Phe	Ile	Pro	Ser	Gly	Phe	Arg	Arg	Ser
				245					250				255		
Met	Asp	Gln	Leu	Phe	Thr	Pro	Ser	Trp	Pro	Arg	Lys	Ala	Lys	Ile	Ala
				260				265				270			
Ile	Gly	Leu	Leu	Glu	Phe	Val	Glu	Asp	Val	Phe	His	Gly	Pro	Tyr	Gly
	275				280						285				
Asn	Phe	Leu	Met	Cys	Asp	Thr	Ser	Ala	Lys	Asn	Leu	Gly	Tyr	Asn	Glu
	290				295					300					
Lys	Tyr	Asp	Leu	Lys	Met	Val	Asp	Met	Arg	Lys	Ile	Val	Pro	Glu	Thr
	305				310				315				320		
Asn	Leu	Lys	Glu	Leu	Ile	Lys	Asp	Arg	His	Cys	Glu	Ser	Asp	Leu	Asp
					325				330				335		
Cys	Val	Tyr	Gly	Thr	Asp	Cys	Arg	Thr	Ser	Cys	Asp	Leu	Ser	Thr	Met
				340				345				350			
Lys	Cys	Thr	Ser	Glu	Val	Ile	Gln	Pro	Asn	Leu	Ala	Lys	Ala	Cys	Gln
	355				360					365					
Leu	Leu	Lys	Asp	Tyr	Leu	Leu	His	Gly	Ala	Pro	Ser	Glu	Ile	Arg	Glu
	370				375					380					
Glu	Leu	Glu	Lys	Gln	Leu	Tyr	Ser	Cys	Ile	Ala	Leu	Lys	Val	Thr	Ala
	385				390				395				400		
Asn	Gln	Met	Glu	Met	Glu	His	Ser	Leu	Ile	Leu	Asn	Asn	Leu	Lys	Thr
				405				410				415			
Leu	Leu	Trp	Lys	Lys	Ile	Ser	Tyr	Thr	Asn	Asp	Ser				
				420				425							

<210> 71

<211> 403

<212> PRT

<213> Homo sapiens

<400> 71

Met	Lys	Tyr	Leu	Phe	Phe	Ser	Trp	Leu	Val	Val	Phe	Val	Gly	Ser	Trp
1				5					10				15		

Ile Ile Tyr Val Gln Tyr Ser Thr Tyr Thr Glu Leu Cys Arg Gly Lys

20	25	30
Asp Cys Lys Lys Ile Ile Cys Asp Lys Tyr Lys Thr Gly Val Ile Asp		
35	40	45
Gly Pro Ala Cys Asn Ser Leu Cys Val Thr Glu Thr Leu Tyr Phe Gly		
50	55	60
Lys Cys Leu Ser Thr Lys Pro Asn Asn Gln Met Tyr Leu Gly Ile Trp		
65	70	75
Asp Asn Leu Pro Gly Val Val Lys Cys Gln Met Glu Gln Ala Leu His		
85	90	95
Leu Asp Phe Gly Thr Glu Leu Glu Pro Arg Lys Glu Ile Val Leu Phe		
100	105	110
Asp Lys Pro Thr Arg Gly Thr Thr Val Gln Lys Phe Lys Glu Met Val		
115	120	125
Tyr Ser Leu Phe Lys Ala Lys Leu Gly Asp Gln Gly Asn Leu Ser Glu		
130	135	140
Leu Val Asn Leu Ile Leu Thr Val Ala Asp Gly Asp Lys Asp Gly Gln		
145	150	155
Val Ser Leu Gly Glu Ala Lys Ser Ala Trp Ala Leu Leu Gln Leu Asn		
165	170	175
Glu Phe Leu Leu Met Val Ile Leu Gln Asp Lys Glu His Thr Pro Lys		
180	185	190
Leu Met Gly Phe Cys Gly Asp Leu Tyr Val Met Glu Ser Val Glu Tyr		
195	200	205
Thr Ser Leu Tyr Gly Ile Ser Leu Pro Trp Val Ile Glu Leu Phe Ile		
210	215	220
Pro Ser Gly Phe Arg Arg Ser Met Asp Gln Leu Phe Thr Pro Ser Trp		
225	230	235
Pro Arg Lys Ala Lys Ile Ala Ile Gly Leu Leu Glu Phe Val Glu Asp		
245	250	255
Val Phe His Gly Pro Tyr Gly Asn Phe Leu Met Cys Asp Thr Ser Ala		
260	265	270
Lys Asn Leu Gly Tyr Asn Asp Lys Tyr Asp Leu Lys Met Val Asp Met		

275	280	285
Arg Lys Ile Val Pro Glu Thr Asn Leu Lys Glu Leu Ile Lys Asp Arg		
290	295	300
His Cys Glu Ser Asp Leu Asp Cys Val Tyr Gly Thr Asp Cys Arg Thr		
305	310	315
Ser Cys Asp Gln Ser Thr Met Lys Cys Thr Ser Glu Val Ile Gln Pro		
325	330	335
Asn Leu Ala Lys Ala Cys Gln Leu Leu Lys Asp Tyr Leu Leu Arg Gly		
340	345	350
Ala Pro Ser Glu Ile Arg Glu Glu Leu Glu Lys Gln Leu Tyr Ser Cys		
355	360	365
Ile Ala Leu Lys Val Thr Ala Asn Gln Met Glu Met Glu His Ser Leu		
370	375	380
Ile Leu Asn Asn Leu Lys Thr Leu Leu Trp Lys Lys Ile Ser Tyr Thr		
385	390	395
Asn Asp Ser		
.		
<210> 72		
<211> 311		
<212> PRT		
<213> Homo sapiens		
<400> 72		
Met Asp Gly Thr Asn Gly Ser Thr Gln Thr His Phe Ile Leu Leu Gly		
1	5	10
15		
Phe Ser Asp Arg Pro His Leu Glu Arg Ile Leu Phe Val Val Ile Leu		
20	25	30
Ile Ala Tyr Leu Leu Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val		
35	40	45
Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala		
50	55	60
His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro Gln		
65	70	75
80		

Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met Gly
85 90 95

Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu Cys
100 105 110

Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys Lys
115 120 125

Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly Leu
130 135 140

Val Ser Val Thr Trp Gly Cys Gly Val Ala Asn Ser Leu Ala Met Ser
145 150 155 160

Pro Val Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp His
165 170 175

Phe Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser Thr Val
180 185 190

Ala Ile Glu Gly Thr Val Phe Val Leu Lys Lys Gly Val Val Leu Ser
195 200 205

Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg Ala Val
210 215 220

Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly Thr Cys
225 230 235 240

Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile Tyr
245 250 255

Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Met Phe Leu
260 265 270

Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro Leu Ile Tyr
275 280 285

Thr Leu Arg Arg Glu Val Lys Gly Ala Leu Gly Arg Leu Leu Leu Gly
290 295 300

Lys Arg Glu Leu Gly Lys Glu
305 310

<210> 73

<211> 314

<212> PRT

<213> Marmota marmota

<400> 73

Met Asp Gly Thr Asn Gly Ser Thr Gln Thr His Phe Ile Leu Leu Gly
1 5 10 15

Phe Ser Asp Arg Pro His Leu Glu Arg Ile Leu Phe Val Val Ile Leu
20 25 30

Ile Ala Tyr Leu Leu Thr Leu Val Gly Asn Thr Thr Ile Ile Leu Val
35 40 45

Ser Arg Leu Asp Pro His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
50 55 60

His Leu Ser Phe Leu Asp Leu Ser Phe Thr Thr Ser Ser Ile Pro Gln
65 70 75 80

Leu Leu Tyr Asn Leu Asn Gly Cys Asp Lys Thr Ile Ser Tyr Met Gly
85 90 95

Cys Ala Ile Gln Leu Phe Leu Phe Leu Gly Leu Gly Gly Val Glu Cys
100 105 110

Leu Leu Leu Ala Val Met Ala Tyr Asp Arg Cys Val Ala Ile Cys Lys
115 120 125

Pro Leu His Tyr Met Val Ile Met Asn Pro Arg Leu Cys Arg Gly Leu
130 135 140

Val Ser Val Thr Trp Gly Cys Gly Val Ala Asn Ser Leu Ala Met Ser
145 150 155 160

Pro Val Thr Leu Arg Leu Pro Arg Cys Gly His His Glu Val Asp His
165 170 175

Phe Leu Arg Glu Met Pro Ala Leu Ile Arg Met Ala Cys Val Ser Thr
180 185 190

Val Ala Ile Glu Gly Thr Val Phe Val Leu Lys Lys Gly Val Val Leu
195 200 205

Ser Pro Leu Val Phe Ile Leu Leu Ser Tyr Ser Tyr Ile Val Arg Ala
210 215 220

Val Leu Gln Ile Arg Ser Ala Ser Gly Arg Gln Lys Ala Phe Gly Thr
225 230 235 240

Cys Gly Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Asn Ile Ile
 245 250 255
 Tyr Met Tyr Met Gln Pro Gly Ala Ser Ser Ser Gln Asp Gln Gly Met
 260 265 270
 Phe Leu Met Leu Phe Tyr Asn Ile Val Thr Pro Leu Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Arg Glu Val Lys Gly Ala Leu Gly Arg Leu
 290 295 300
 Leu Leu Gly Lys Arg Glu Leu Gly Lys Glu
 305 310

 <210> 74
 <211> 320
 <212> PRT
 <213> Homo sapiens

 <400> 74
 Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
 1 5 10 15
 Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
 20 25 30
 Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
 35 40 45
 Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
 50 55 60
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
 65 70 75 80
 Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
 85 90 95
 Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
 100 105 110
 Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
 115 120 125
 Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met

130	135	140
Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys		
145	150	155
Thr Leu Thr Leu Asn Leu Pro Thr Cys Gly Asn Asn Ile Leu Asp His		
165	170	175
Phe Leu Cys Glu Leu Pro Ala Leu Val Lys Ile Ala Cys Val Asp Thr		
180	185	190
Thr Thr Val Glu Met Ser Val Phe Ala Leu Gly Ile Ile Ile Val Leu		
195	200	205
Thr Pro Leu Ile Leu Ile Ser Tyr Gly Tyr Ile Ala Lys Ala		
210	215	220
Val Leu Arg Thr Lys Ser Lys Ala Ser Gln Arg Lys Ala Met Asn Thr		
225	230	235
Cys Gly Ser His Leu Thr Val Val Ser Met Phe Tyr Gly Thr Ile Ile		
245	250	255
Tyr Met Tyr Leu Gln Pro Gly Asn Arg Ala Ser Lys Asp Gln Gly Lys		
260	265	270
Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu		
275	280	285
Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu		
290	295	300
Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys Lys Ser		
305	310	315
320		
<210> 75		
<211> 320		
<212> PRT		
<213> Homo sapiens		
<400> 75		
Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly		
1	5	10
15		

Phe	Ser	Asn	His	Pro	Lys	Met	Glu	Met	Ile	Leu	Ser	Gly	Val	Val	Ala
									20					30	
Ile	Phe	Tyr	Leu	Ile	Thr	Leu	Val	Gly	Asn	Thr	Ala	Ile	Ile	Leu	Ala
									35					45	
Ser	Leu	Leu	Asp	Ser	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Arg
									50					60	
Asn	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Thr	Ser	Ile	Ile	Pro	Gln
									65					80	
Val	Leu	Val	Asn	Leu	Trp	Gly	Pro	Asp	Lys	Thr	Ile	Ser	Tyr	Val	Gly
									85					95	
Cys	Ile	Ile	Gln	Leu	Tyr	Val	Tyr	Met	Trp	Leu	Gly	Ser	Val	Glu	Cys
									100					110	
Leu	Leu	Leu	Ala	Val	Met	Ser	Tyr	Asp	Arg	Phe	Thr	Ala	Ile	Cys	Lys
									115					125	
Pro	Leu	His	Tyr	Phe	Val	Val	Met	Asn	Pro	His	Leu	Cys	Leu	Lys	Met
									130					140	
Ile	Ile	Met	Ile	Trp	Ser	Ile	Ser	Leu	Ala	Asn	Ser	Val	Val	Leu	Cys
									145					160	
Thr	Leu	Thr	Leu	Asn	Leu	Pro	Thr	Cys	Gly	Asn	Asn	Ile	Leu	Asp	His
									165					175	
Phe	Leu	Cys	Glu	Leu	Pro	Ala	Leu	Val	Lys	Ile	Ala	Cys	Val	Asp	Thr
									180					190	
Thr	Thr	Val	Glu	Met	Ser	Val	Phe	Ala	Leu	Gly	Ile	Ile	Ile	Val	Leu
									195					205	
Thr	Pro	Leu	Ile	Leu	Ile	Leu	Ile	Ser	Tyr	Gly	Tyr	Ile	Ala	Lys	Ala
									210					220	
Val	Leu	Arg	Thr	Lys	Ser	Lys	Ala	Ser	Gln	Arg	Lys	Ala	Met	Asn	Thr
									225					240	
Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ser	Met	Phe	Tyr	Gly	Thr	Ile	Ile
									245					255	
Tyr	Met	Tyr	Leu	Gln	Pro	Gly	Asn	Arg	Ala	Ser	Lys	Asp	Gln	Gly	Lys
									260					270	

Phe Leu Thr Leu Phe Tyr Thr Val Ile Thr Pro Ser Leu Asn Pro Leu
275 280 285

Ile Tyr Thr Leu Arg Asn Lys Asp Met Lys Asp Ala Leu Lys Lys Leu
290 295 300

Met Arg Phe His His Lys Ser Thr Lys Ile Lys Arg Asn Cys Lys Ser
305 310 315 320

<210> 76
<211> 320
<212> PRT
<213> Homo sapiens

<400> 76
Met Asp Gln Ser Asn Tyr Ser Ser Leu His Gly Phe Ile Leu Leu Gly
1 5 10 15

Phe Ser Asn His Pro Lys Met Glu Met Ile Leu Ser Gly Val Val Ala
20 25 30

Ile Phe Tyr Leu Ile Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Ala
35 40 45

Ser Leu Leu Asp Ser Gln Leu His Thr Pro Met Tyr Phe Phe Leu Arg
50 55 60

Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Ile Ile Pro Gln
65 70 75 80

Met Leu Val Asn Leu Trp Gly Pro Asp Lys Thr Ile Ser Tyr Val Gly
85 90 95

Cys Ile Ile Gln Leu Tyr Val Tyr Met Trp Leu Gly Ser Val Glu Cys
100 105 110

Leu Leu Leu Ala Val Met Ser Tyr Asp Arg Phe Thr Ala Ile Cys Lys
115 120 125

Pro Leu His Tyr Phe Val Val Met Asn Pro His Leu Cys Leu Lys Met
130 135 140

Ile Ile Met Ile Trp Ser Ile Ser Leu Ala Asn Ser Val Val Leu Cys
145 150 155 160

Thr	Leu	Thr	Leu	Asn	Leu	Pro	Thr	Cys	Gly	Asn	Asn	Ile	Leu	Asp	His
														175	
Phe	Leu	Cys	Glu	Leu	Pro	Ala	Leu	Val	Lys	Ile	Ala	Cys	Val	Asp	Thr
														190	
Thr	Thr	Val	Glu	Met	Ser	Val	Phe	Ala	Leu	Gly	Ile	Ile	Ile	Val	Leu
														205	
Thr	Pro	Leu	Ile	Leu	Ile	Leu	Ile	Ser	Tyr	Gly	Tyr	Ile	Ala	Lys	Ala
														220	
Val	Leu	Arg	Thr	Lys	Ser	Lys	Ala	Ser	Gln	Arg	Lys	Ala	Met	Asn	Thr
														240	
Cys	Gly	Ser	His	Leu	Thr	Val	Val	Ser	Met	Phe	Tyr	Gly	Thr	Ile	Ile
														255	
Tyr	Met	Tyr	Leu	Gln	Pro	Gly	Asn	Arg	Ala	Ser	Lys	Asp	Gln	Gly	Lys
														270	
Phe	Leu	Thr	Leu	Phe	Tyr	Thr	Val	Ile	Thr	Pro	Ser	Leu	Asn	Pro	Leu
														285	
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asn	Met	Lys	Asp	Ala	Leu	Lys	Lys	Leu
														300	
Met	Arg	Phe	His	His	Lys	Ser	Thr	Lys	Ile	Lys	Arg	Asn	Cys	Lys	Ser
														320	

<210> 77

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 7tm_1, 7
transmembrane receptor domain sequence

<400> 77

Gly Asn Leu Leu Val Ile Leu Val Ile Leu Arg Thr Lys Lys Leu Arg

1

5

10

15

<210> 78
<211> 188

<212> PRT

<213> Homo sapiens

<400> 78

Met Thr Ala Pro Ser Cys Ala Phe Pro Val Gln Phe Arg Gln Pro Ser
1 5 10 15

Val Ser Gly Leu Ser Gln Ile Thr Lys Ser Leu Tyr Ile Ser Asn Gly
20 25 30

Val Ala Ala Asn Asn Lys Leu Met Leu Ser Ser Asn Gln Ile Thr Met
35 40 45

Val Ile Asn Val Ser Val Glu Val Val Asn Thr Leu Tyr Glu Asp Ile
50 55 60

Gln Tyr Met Gln Val Pro Val Ala Asp Ser Pro Asn Ser Arg Leu Cys
65 70 75 80

Asp Phe Phe Asp Pro Ile Ala Asp His Ile His Ser Val Glu Met Lys
85 90 95

Gln Gly Arg Thr Leu Leu His Cys Ala Ala Gly Val Ser Arg Ser Ala
100 105 110

Ala Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ala Met Ser Leu Leu
115 120 125

Asp Ala His Thr Trp Thr Lys Ser Cys Arg Pro Ile Ile Arg Pro Asn
130 135 140

Ser Gly Phe Trp Glu Gln Leu Ile His Tyr Glu Phe Gln Leu Phe Gly
145 150 155 160

Lys Asn Thr Val His Met Val Ser Ser Pro Val Gly Met Ile Pro Asp
165 170 175

Ile Tyr Glu Lys Glu Val Arg Leu Met Ile Pro Leu
180 185

<210> 79

<211> 188

<212> PRT

<213> Mus musculus

<400> 79

Met Thr Ser Pro Trp Ser Ala Phe Pro Val Gln Ile Pro Gln Pro Ser

1

5

10

15

Ile Arg Gly Leu Ser Gln Ile Thr Lys Ser Leu Phe Ile Ser Asn Gly
20 25 30

Val Ala Ala Asn Asn Lys Leu Leu Ser Ser Asn Gln Ile Thr Thr
35 40 45

Val Ile Asn Val Ser Val Glu Val Ala Asn Thr Phe Tyr Glu Asp Ile
50 55 60

Gln Tyr Val Gln Val Pro Val Val Asp Ala Pro Val Ala Arg Leu Ser
65 70 75 80

Asn Phe Phe Asp Ser Val Ala Asp Arg Ile His Ser Val Glu Met Gln
85 90 95

Lys Gly Arg Thr Leu Leu His Cys Ala Ala Gly Val Ser Arg Ser Ala
100 105 110

Ala Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ala Met Ser Leu Val
115 120 125

Asp Ala His Thr Trp Thr Lys Ser Cys Arg Pro Ile Ile Arg Pro Asn
130 135 140

Ser Gly Phe Trp Glu Gln Leu Ile His Tyr Glu Leu Gln Leu Phe Gly
145 150 155 160

Lys Asn Thr Met Gln Met Met Asp Ser Pro Met Gly Arg Ile Pro Asp
165 170 175

Ile Tyr Glu Lys Glu Thr Arg Leu Met Ile Pro Leu
180 185

<210> 80

<211> 151

<212> PRT

<213> Homo sapiens

<400> 80

Ala Arg Gly Leu Ser Ser Asn Gln Ile Thr Met Val Ile Asn Val Ser
1 5 10 15

Val Glu Val Val Asn Thr Leu Tyr Glu Asp Ile Gln Tyr Met Gln Val
20 25 30

Pro Val Ala Asp Ser Pro Asn Ser Arg Leu Cys Asp Phe Phe Asp Pro
35 40 45

Ile Ala Asp His Ile His Ser Val Glu Met Lys Gln Gly Arg Thr Leu
50 55 60

Leu His Cys Ala Ala Gly Val Ser Arg Ser Ala Ala Leu Cys Leu Ala
65 70 75 80

Tyr Leu Met Lys Tyr His Ala Met Ser Leu Leu Asp Ala His Thr Trp
85 90 95

Thr Lys Ser Cys Arg Pro Ile Ile Arg Pro Asn Ser Gly Phe Trp Glu
100 105 110

Gln Leu Ile His Tyr Glu Phe Gln Leu Phe Gly Lys Asn Thr Val His
115 120 125

Met Val Ser Ser Pro Val Gly Met Ile Pro Asp Ile Tyr Glu Lys Glu
130 135 140

Val Arg Leu Met Ile Pro Leu
145 150

<210> 81

<211> 187

<212> PRT

<213> Mus musculus

<400> 81

Met Thr Thr Ala Ser Cys Ile Phe Pro Ser Gln Ala Thr Gln Gln Asp
1 5 10 15

Asn Ile Tyr Gly Leu Ser Gln Ile Thr Ala Ser Leu Phe Ile Ser Asn
20 25 30

Ser Ala Val Ala Asn Asp Lys Leu Thr Leu Ser Asn Asn His Ile Thr
35 40 45

Thr Ile Ile Asn Val Ser Ala Glu Val Val Asn Thr Phe Phe Glu Asp
50 55 60

Ile Gln Tyr Val Gln Val Pro Val Ser Asp Ala Pro Asn Ser Tyr Leu
65 70 75 80

Tyr Asp Phe Phe Asp Pro Ile Ala Asp Ile His Gly Val Glu Met Arg
85 90 95

Asn Gly Arg Thr Leu Leu His Cys Ala Ala Gly Val Ser Arg Ser Ala
100 105 110

Thr Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Asn Met Thr Leu Leu
115 120 125

Asp Ala His Thr Trp Thr Lys Thr Cys Arg Pro Ile Ile Arg Pro Asn
130 135 140

Asn Gly Phe Trp Glu Gln Leu Ile His Tyr Glu Phe Lys Leu Phe Ser
145 150 155 160

Arg Asn Thr Val Arg Met Ile Tyr Ser Pro Ile Gly Leu Ile Pro Asn
165 170 175

Ile Tyr Glu Lys Ala Tyr Leu Met Glu Leu Met
180 185

<210> 82

<211> 190

<212> PRT

<213> Homo sapiens

<400> 82

Met Thr Ala Ser Ala Ser Ser Phe Ser Ser Ser Gln Gly Val Gln Gln
1 5 10 15

Pro Ser Ile Tyr Ser Phe Ser Gln Ile Thr Arg Ser Leu Phe Leu Ser
20 25 30

Asn Gly Val Ala Ala Asn Asp Lys Leu Leu Leu Ser Ser Asn Arg Ile
35 40 45

Thr Ala Ile Val Asn Ala Ser Val Glu Val Val Asn Val Phe Phe Glu
50 55 60

Gly Ile Gln Tyr Ile Lys Val Pro Val Thr Asp Ala Arg Asp Ser Arg
65 70 75 80

Leu Tyr Asp Phe Phe Asp Pro Ile Ala Asp Leu Ile His Thr Ile Asp
85 90 95

Met Arg Gln Gly Arg Thr Leu Leu His Cys Met Ala Gly Val Ser Arg
100 105 110

Ser Ala Ser Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ser Met Ser

115 120 125

Leu Leu Asp Ala His Thr Trp Thr Lys Ser Arg Arg Pro Ile Ile Arg
130 135 140

Pro Asn Asn Gly Phe Trp Glu Gln Leu Ile Asn Tyr Glu Phe Lys Leu
145 150 155 160

Phe Asn Asn Asn Thr Val Arg Met Ile Asn Ser Pro Val Gly Asn Ile
165 170 175

Pro Asp Ile Tyr Glu Lys Asp Leu Arg Met Met Ile Ser Met
180 185 190

<210> 83
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: DSPc, Dual
specificity phosphatase domain sequence

<400> 83
Gly Pro Ser Glu Ile Leu Pro His Leu Tyr Leu Gly Ser Tyr Ser Asp
1 5 10 15

Ala Ser Asn Leu Ala Leu Lys Lys Leu Gly Ile Thr His Val Ile
20 25 30

Asn Val Thr Glu Glu Val Pro Asn Ser Asn Lys Ser Gly Phe Leu Tyr
35 40 45

Leu Gly Ile Pro Val Asp Asp Asn Thr Glu Thr Lys Ile Ser Pro Tyr
50 55 60

Leu Pro Glu Ala Val Glu Phe Ile Glu Asp Ala Glu Lys Lys Gly Gly
65 70 75 80

Lys Val Leu Val His Cys Gln Ala Gly Val Ser Arg Ser Ala Thr Leu
85 90 95

Ile Ile Ala Tyr Leu Met Lys Tyr Arg Asn Met Ser Leu Asn Asp Ala
100 105 110

Tyr Asp Phe Val Lys Glu Arg Arg Pro Ile Ile Ser Pro Asn Phe Gly
115 120 125

Phe Leu Arg Gln Leu Ile Glu Tyr Glu Arg Lys
130 135

<210> 84
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Description of
Artificial Sequence: DSPc, Dual specificity
phosphatase domain sequence

<400> 84
Gly Pro Ser Glu Ile Leu Pro His Leu Tyr Leu Gly Ser Tyr Pro Thr
1 5 10 15
Ala Ser Asn Leu Ala Phe Leu Ser Lys Leu Gly Ile Thr His Val Ile
20 25 30
Asn Val Thr Glu Glu Val Pro Asn Ser Lys Asn Ser Gly Phe Leu Tyr
35 40 45
Leu His Ile Pro Val Asp Asp Asn His Glu Thr Asp Ile Ser Pro Tyr
50 55 60
Leu Asp Glu Ala Val Glu Phe Ile Glu Asp Ala Arg Gln Lys Gly Gly
65 70 75 80
Lys Val Leu Val His Cys Gln Ala Gly Ile Ser Arg Ser Ala Thr Leu
85 90 95
Ile Ile Ala Tyr Leu Met Lys Thr Arg Asn Leu Ser Leu Asn Glu Ala
100 105 110
Tyr Ser Phe Val Lys Glu Arg Arg Pro Ile Ile Ser Pro Asn Phe Gly
115 120 125
Phe Lys Arg Gln Leu Ile Glu Tyr Glu Arg Lys
130 135

<210> 85
<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PTpC, Protein
tyrosine phosphatase domain sequence

<400> 85
Arg Lys Ser Gln Ser Thr Leu Arg Asn Ser Gly Pro Ile Val Val His
1 5 10 15

Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Ile Ala Ile Asp Ile
20 25 30

Leu

<210> 86
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
sequence

<400> 86
ctggaccgaa gctacagcta ta 22

<210> 87
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
sequence

<400> 87

atggcccaagg cccattctac aataaa

26

<210> 88
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer sequence

<400> 88

cgagctcctc ttcagagatg a

21

<210> 89

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer sequence

<400> 89

gctccttcaa gacggtgtat c

21

<210> 90

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer sequence

<400> 90

ctagacacccg acaccacagt ggaggt

26

<210> 91

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer sequence

<400> 91

ccgctcagct ctagacagtt t

21

<210> 92

<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer sequence

<400> 92
gtaaaaggcat ctccacacctga ct 22

<210> 93
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer sequence

<400> 93
tcacttccat ccagggccac tgg 23

<210> 94
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer sequence

<400> 94
gggctaatat cagctggaat tc 22

<210> 95
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer sequence

<400> 95
aattgtttgg caagaacact gt 22

<210> 96
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
sequence

<400> 96
ccagtggaa tgatccctga catcta

26

<210> 97
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer
sequence

<400> 97
atcatcaaac ggacttcctt ct

22